GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 20:41:41 ; Search time 836 Seconds
(without alignments)
10304.187 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgaattcgaaatc.....ttgataaaagtgggtattaa 1641

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1641	100.0	1641	5	AAS01082	Aas01082 Arabidops
2		1622	98.8	1902	12	ADF47823	Adf47823 Arabidops
3		271.8	16.6	3896	3	AAC64438	Aac64438 Arabidops
4		271.8	16.6	3896	3	AAC64448	Aac64448 Arabidops
5		176.2	10.7	328	5	AAS01096	Aas01096 Corn ster
6		110.4	6.7	709	3	AAC64449	Aac64449 Lycopersi
7		110.4	6.7	709	3	AAC64439	Aac64439 Lycopersi
8		109	6.6	356	5	AAS01097	Aas01097 Corn ster
9		52.6	3.2	1872	12	ADF47831	Adf47831 Schizosac
10		49.4	3.0	1701	12	ADF47817	Adf47817 Yeast mem
11		49.4	3.0	1986	3	AAC64431	Aac64431 Saccharom
12		49.4	3.0	1986	3	AAC64441	Aac64441 Saccharom
13		49.4	3.0	1986	3	AAC64440	Aac64440 Saccharom
14		49.4	3.0	1986	5	AAS01342	Aas01342 Yeast LCA
15		49.4	3.0	1986	12	ADF47816	Adf47816 Yeast acy
16	c	49.4	3.0	2000	8	ADA71938	Ada71938 Rice gene
17		47.4	2.9	2000	8	ADA71938	Ada71938 Rice gene
18		47.4	2.9	2312	3	AAC64442	Aac64442 Schizosac
19		47.4	2.9	2312	3	AAC64432	Aac64432 Schizosac
20		40.6	2.5	110000	2	AAV21209_12	Continuation (13 o
21		39.4	2.4	2223	12	ADF47830	Adf47830 Aspergill
22	c	38.8	2.4	486	4	AAF75507	Aaf75507 Polygluta
23		38.2	2.3	2047	12	ADF47829	Adf47829 Aspergill
24		37.6	2.3	473	6	ABV94819	Abv94819 Human pan
25		37.6	2.3	1292	10	ADC78228	Adc78228 Human sec
26		37.6	2.3	2329	10	ADG32012	Adg32012 Human DNA
27		37.6	2.3	3556	12	ADH22401	Adh22401 Human cDN
28		37.6	2.3	3737	6	AAS94885	Aas94885 Human DNA
29	c	37.6	2.3	11477	4	ABL17946	Abl17946 Drosophil
30	c	37.6	2.3	12600	4	ABL17948	Abl17948 Drosophil
31	c	37.6	2.3	12600	4	ABL17952	Abl17952 Drosophil
32	c	37.6	2.3	12600	4	ABL27368	Abl27368 Drosophil
33		36.4	2.2	296	5	ABV18850	Abv18850 Human pro
34		36.4	2.2	110000	6	ABA90521_16	Continuation (17 o
35		36	2.2	2433	9	AAL62907	Aal62907 Rice cDNA
36	c	36	2.2	3579	3	AAA70099	Aaa70099 Plasmodiu
37		35.8	2.2	2016	12	ADF47833	Adf47833 Crepis pa
38		35.8	2.2	2976	4	ABA03653	Aba03653 Murine A-
39	c	35.8	2.2	4590	5	AAH24065	Aah24065 Yeast AOD
40	c	35.8	2.2	266145	10	ADE87477	Ade87477 Fowlpox v
41		35.6	2.2	2356	6	AAS62537	Aas62537 cDNA sequ
42		35.6	2.2	4089	4	AAL37519	Aal37519 Human mus
43		35.6	2.2	4089	8	ABX60507	Abx60507 cDNA enco
44		35.6	2.2	4089	12	ADJ31257	Adj31257 Human mus
45	c	35.6	2.2	17703	6	ABK39953	Abk39953 Human che

ALIGNMENTS

RESULT 1
AAS01082
ID AAS01082 standard; DNA; 1641 BP.
XX
AC AAS01082;
XX
DT 31-MAY-2001 (first entry)
XX
DE Arabidopsis thaliana sterol acyltransferase LCAT2 DNA.
XX
KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW nutritional supplement; dairy product; food product; salad dressing; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1. .1641
FT /*tag= a
FT /product= "LCAT2"
XX
PN WO200116308-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023863.
XX
PR 30-AUG-1999; 99US-0152493P.
XX
PA (MONS) MONSANTO CO.
XX
PI Lassner M, Van Eenennaam A;
XX
DR WPI; 2001-169010/17.
DR P-PSDB; AAU00459.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT -like polypeptides, for modifying the sterol content and oil production
PT of plants.
XX
PS Claim 5; Page 77; 127pp; English.
XX
CC The present sequence encodes for Arabidopsis thaliana

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CC   lecithin:cholesterol acyltransferase-like 2 (LCAT2). Several novel
CC   polynucleotides encoding the plant sterol acyltransferases LCAT
CC   (AAS001081-AAS01104, AAS01341) and ACAT (acyl CoA:cholesterol
CC   acyltransferase-like; AAS01311-AAS01319) are described. A yeast LCAT
CC   related open reading frame, LRO1 gene sequence (AAS01342), and a rat ACAT
CC   (AAS01105) cDNA sequence are also described. The polynucleotides encoding
CC   LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also
CC   be used in a recombinant construct to transform a host cell (preferably
CC   of a plant) or a plant. The recombinant construct is used to increase or
CC   decrease the sterol content of the host cell or plant. It can be used to
CC   alter oil production of the cell or plant, preferably by increasing it.
CC   The oil of the plant or the plant itself is used as a food product, or as
CC   nutritional or dietary supplements, or in pharmaceutical compositions for
CC   lowering cholesterol. The oil can be used in foods e.g. margarine,
CC   butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,
CC   cheese, processed meat, pasta, sauces, cereals, desserts, dips, chips,
CC   baked goods, pastries, cookies, snack bars, confections, chocolates, and
CC   beverages. The alteration in sterol content and/or composition can also
CC   provide a plant with tolerance to stress and insect damage
XX
SQ   Sequence 1641 BP; 438 A; 355 C; 378 G; 470 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1641;  DB 5;  Length 1641;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1641;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420

Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480

Qy        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540

Qy        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600

Qy        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660

Qy        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720

Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780

Qy        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840

Qy        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900

Qy        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960

Qy        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140

Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200

Qy       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260

Qy       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320

Qy       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380

Qy       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440

Qy       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500

Qy       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560

Qy       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620

Qy       1621 CTTGATAAAAGTGGGTATTAA 1641
              |||||||||||||||||||||
Db       1621 CTTGATAAAAGTGGGTATTAA 1641


RESULT 2
ADF47823
ID   ADF47823 standard; DNA; 1902 BP.
XX
AC   ADF47823;
XX
DT   26-FEB-2004  (first entry)
```

XX
DE Arabidopsis thaliana acyltransferase nucleotide sequence SEQ ID NO:8.
XX
KW acyltransferase; enzyme; membrane-spanning region;
KW active membrane independent acyltransferase; fatty acid ester;
KW fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003100044-A1.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-SE000870.
XX
PR 29-MAY-2002; 2002SE-00001581.
PR 29-MAY-2002; 2002US-0383889P.
PR 20-JAN-2003; 2003SE-00000142.
XX
PA (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;
XX
DR WPI; 2004-053268/05.
DR P-PSDB; ADF47824.
XX
PT New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT useful for producing structured lipids or fat-soluble molecules, in
PT removing undesirable fat or in modifying lipids in animal or plant raw
PT material.
XX
PS Claim 5; SEQ ID NO 8; 91pp; English.
XX
CC The present invention describes a nucleotide sequence (I) derived from a
CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC least one membrane-spanning region. (I) encodes an improved active
CC membrane independent acyltransferase polypeptide in which at least one
CC amino acid residue of the membrane-spanning region has been deleted
CC and/or substituted as compared to the original acyltransferase
CC polypeptide, where the encoded active membrane independent
CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC acid thioesters such as triacylglycerols, diacylglycerols,
CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC ; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridising to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 1902 BP; 516 A; 405 C; 444 G; 537 T; 0 U; 0 Other;

Query Match 98.8%; Score 1622; DB 12; Length 1902;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1625; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTGCGGTGGCCGAACGGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420

Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTGAGTTTGGTGTAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480

Qy        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540

Qy        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600

Qy        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660

Qy        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720

Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780

Qy        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840

Qy        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900

Qy        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960

Qy        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGAATGTGGCCTCCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
```

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Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200

Qy       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260

Qy       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTATGAAACTGAA 1320

Qy       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380

Qy       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440

Qy       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500

Qy       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560

Qy       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620

Qy       1621 CTTGATAAAA 1630
             ||||||||||
Db       1621 CTTGATAAAA 1630
```

RESULT 3
AAC64438
ID AAC64438 standard; DNA; 3896 BP.
XX
AC AAC64438;
XX
DT 12-FEB-2001 (first entry)
XX
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200060095-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-EP002701.
XX
PR 01-APR-1999; 99EP-00106656.
PR 10-JUN-1999; 99EP-00111321.
PR 07-FEB-2000; 2000US-0180687P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Stymne S;
XX
DR WPI; 2000-665012/64.
XX
PT Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful for
PT producing triacylglycerol, or for transforming any cell or organism to
PT increase oil content.
XX
PS Claim 6; Page 60-61; 97pp; English.
XX
CC The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC independent reaction) the transfer of fatty acids from phospholipids to
CC diacylglycerol in the biosynthetic pathway for the production of
CC triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC nucleotides encoding them are useful for producing TAG and/or TAG with
CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC transforming any cell or organism in order to be expressed in this cell
CC or organism and result in an altered, preferably increased oil content of
CC this cell or organism. The present sequence represents the Arabidopsis
CC thaliana PDAT genomic DNA
XX
SQ Sequence 3896 BP; 1042 A; 725 C; 769 G; 1360 T; 0 U; 0 Other;

```
  Query Match             16.6%;  Score 271.8;  DB 3;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 1.6e-74;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TCAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 1846

Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1847 TTCAAAGAATTGCAAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAA 1906

Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 1966

Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------- 987
              |||||||||||||||||||||||||||||||||||||
Db       1967 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 2026

Qy        988 ---------- 987

Db       2027 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 2086

Qy        988 ----------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
                        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 2146

Qy       1036 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 2206

Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 2255
```

RESULT 4
AAC64448
ID AAC64448 standard; DNA; 3896 BP.
XX
AC AAC64448;
XX
DT 12-FEB-2001 (first entry)
XX
DE Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10b.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200060095-A2.
XX
PD 12-OCT-2000.
XX

```
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 95-96; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the Arabidopsis
CC   thaliana PDAT genomic DNA
XX
SQ   Sequence 3896 BP; 1042 A; 733 C; 760 G; 1360 T; 0 U; 1 Other;

  Query Match             16.6%;  Score 271.8;  DB 3;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 1.6e-74;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 TCAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 1846

Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1847 TTCAAAGAATTGCAAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAA 1906

Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 1966

Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------------------- 987
              |||||||||||||||||||||||||||||||||||||||
Db       1967 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 2026

Qy        988 ------------------------------------------------------------ 987

Db       2027 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 2086

Qy        988 ------------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
                          |||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 2146

Qy       1036 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2147 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 2206

Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db       2207 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 2255


RESULT 5
AAS01096
ID   AAS01096 standard; cDNA; 328 BP.
XX
AC   AAS01096;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Corn sterol acyltransferase LCAT EST sequence #3.
XX
KW   Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW   acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW   nutritional supplement; dairy product; food product; salad dressing;
KW   corn; Arabidopsis thaliana; expressed sequence tag; EST; ss.
XX
OS   Zea mays.
XX
PN   WO200116308-A2.
XX
PD   08-MAR-2001.
XX
PF   30-AUG-2000; 2000WO-US023863.
XX
PR   30-AUG-1999;   99US-0152493P.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Lassner M,  Van Eenennaam A;
XX
DR   WPI; 2001-169010/17.
XX
PT   New isolated nucleic acid encoding plant lecithin:cholesterol
PT   acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT   -like polypeptides, for modifying the sterol content and oil production
PT   of plants.
XX
PS   Claim 5; Page 90; 127pp; English.
XX
CC   The present sequence for corn LCAT (lecithin:cholesterol acyltransferase-
CC   like) EST sequence #3 is closely related to the Arabidopsis thaliana
CC   LCAT2 sequence. Several novel polynucleotides encoding the plant sterol
CC   acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT (acyl
CC   CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are described. A
CC   yeast LCAT related open reading frame, LRO1 gene sequence (AAS01342), and
CC   a rat ACAT (AAS01105) cDNA sequence are also described. The
CC   polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
CC   polypeptides. They can also be used in a recombinant construct to
CC   transform a host cell (preferably of a plant) or a plant. The recombinant
CC   construct is used to increase or decrease the sterol content of the host
CC   cell or plant. It can be used to alter oil production of the cell or
CC   plant, preferably by increasing it. The oil of the plant or the plant
CC   itself is used as a food product, or as nutritional or dietary
CC   supplements, or in pharmaceutical compositions for lowering cholesterol.
CC   The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC   dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC   pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
CC   cookies, snack bars, confections, chocolates, and beverages. The
CC   alteration in sterol content and/or composition can also provide a plant
CC   with tolerance to stress and insect damage
XX
SQ   Sequence 328 BP; 86 A; 68 C; 73 G; 101 T; 0 U; 0 Other;

  Query Match             10.7%;  Score 176.2;  DB 5;  Length 328;
  Best Local Similarity   79.0%;  Pred. No. 8.1e-45;
  Matches  222;  Conservative    0;  Mismatches   58;  Indels    1;  Gaps    1;

Qy        238 ACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAAT 297
              ||   |||| | ||||| || || |||||| |||| || ||| |||| || || ||||||
Db         35 ACATTGCTTTTCTCTGCGGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAAT 94

Qy        298 CAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAA 357
              || | ||||||||||||| || |||||| ||||||| ||||||| ||| || || |||||
Db         95 CAGATAGACCATCCCGAATGCAAGTCAAGGCCTGATAGTGGTC-TTCTGCAATTACAGAG 153

Qy        358 TTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGG 417
              |||| || ||||| |||||||||||||| ||| | || |||||||| ||| | || |||
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Db        154 CTGGACCCTGGTTATATAACAGGTCCTCTCTCTTCAGTATGGAAAGAATGGGTCAAATGG 213

Qy        418 TGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTG 477
              ||||| |||||||| || ||||| ||||||||| |||||||||| || |||||||||| ||
Db        214 TGTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCGTATGATTGGAGACTG 273

Qy        478 TCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAA 518
              | ||| | |    | || ||| | || || ||||||||||
Db        274 CCCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAA 314


RESULT 6
AAC64449
ID   AAC64449 standard; cDNA; 709 BP.
XX
AC   AAC64449;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Lycopersicon esculentum PDAT nucleotide sequence SEQ ID NO:11b.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ss.
XX
OS   Lycopersicon esculentum.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 97; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the Lycopersicon
CC   esculentum PDAT nucleotide sequence
XX
SQ   Sequence 709 BP; 226 A; 121 C; 161 G; 201 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 110.4;  DB 3;  Length 709;
  Best Local Similarity   74.5%;  Pred. No. 9.5e-24;
  Matches  152;  Conservative    0;  Mismatches   51;  Indels    1;  Gaps    1;

Qy       1426 CTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTA 1485
              || || || ||||| |||||||||| | | || ||| |||| || ||| |    || |||
Db          1 CTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAGCATGAT-GTTCAGATGTA 59

Qy       1486 CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA 1545
              || ||| | |||||| | || ||| | |||||   ||| |||||  | || ||||||||
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```
Db         60 CAAGTGCATCTAAATATAGAGCATCAACATGGTGAAGATATCATTCCCAATATGACAAAG 119

Qy       1546 GCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGA 1605
                ||| |   | |||||||||||| |||||| || ||||| ||  |||| ||||  |||
Db         120 TTACCTACAATGAAGTACATAACCTATTATGAGGATTCTGAAAGTTTTCCAGGGACAAGA 179

Qy       1606 ACCGCAGTCTGGGAGCTTGATAAA 1629
              || ||||| ||||||||||||||
Db         180 ACAGCAGTTTGGGAGCTTGATAAA 203


RESULT 7
AAC64439
ID   AAC64439 standard; cDNA; 709 BP.
XX
AC   AAC64439;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Lycopersicon esculentum PDAT nucleotide sequence SEQ ID NO:12.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ss.
XX
OS   Lycopersicon esculentum.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 62; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the Lycopersicon
CC   esculentum PDAT nucleotide sequence
XX
SQ   Sequence 709 BP; 226 A; 120 C; 162 G; 201 T; 0 U; 0 Other;

  Query Match             6.7%;  Score 110.4;  DB 3;  Length 709;
  Best Local Similarity   74.5%;  Pred. No. 9.5e-24;
  Matches  152;  Conservative    0;  Mismatches   51;  Indels    1;  Gaps    1;

Qy       1426 CTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTA 1485
              || || || ||||| |||||||||| | | || ||| |||| || ||| |    || |||
Db          1 CTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAGCATGAT-GTTCAGATGTA 59

Qy       1486 CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA 1545
              || ||| | |||||| | || ||| | |||||   ||| |||||  | || ||||||||
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```
Db         60 CAAGTGCATCTAAATATAGAGCATCAACATGGTGAAGATATCATTCCCAATATGACAAAG 119

Qy       1546 GCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGA 1605
              ||| |   | |||||||||||||| |||||| || ||||| ||  |||| ||||  |||
Db        120 TTACCTACAATGAAGTACATAACCTATTATGAGGATTCTGAAAGTTTTCCAGGGACAAGA 179

Qy       1606 ACCGCAGTCTGGGAGCTTGATAAA 1629
              || ||||| ||||||||||||||||
Db        180 ACAGCAGTTTGGGAGCTTGATAAA 203


RESULT 8
AAS01097
ID   AAS01097 standard; cDNA; 356 BP.
XX
AC   AAS01097;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Corn sterol acyltransferase LCAT EST sequence #4.
XX
KW   Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW   acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW   nutritional supplement; dairy product; food product; salad dressing;
KW   corn; Arabidopsis thaliana; expressed sequence tag; EST; ss.
XX
OS   Zea mays.
XX
PN   WO200116308-A2.
XX
PD   08-MAR-2001.
XX
PF   30-AUG-2000; 2000WO-US023863.
XX
PR   30-AUG-1999;   99US-0152493P.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Lassner M,  Van Eenennaam A;
XX
DR   WPI; 2001-169010/17.
XX
PT   New isolated nucleic acid encoding plant lecithin:cholesterol
PT   acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT   -like polypeptides, for modifying the sterol content and oil production
PT   of plants.
XX
PS   Claim 5; Page 90; 127pp; English.
XX
CC   The present sequence for corn LCAT (lecithin:cholesterol acyltransferase-
CC   like) EST sequence #4 is closely related to the Arabidopsis thaliana
CC   LCAT2 sequence. Several novel polynucleotides encoding the plant sterol
CC   acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT (acyl
CC   CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are described. A
CC   yeast LCAT related open reading frame, LRO1 gene sequence (AAS01342), and
CC   a rat ACAT (AAS01105) cDNA sequence are also described. The
CC   polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
CC   polypeptides. They can also be used in a recombinant construct to
CC   transform a host cell (preferably of a plant) or a plant. The recombinant
CC   construct is used to increase or decrease the sterol content of the host
CC   cell or plant. It can be used to alter oil production of the cell or
CC   plant, preferably by increasing it. The oil of the plant or the plant
CC   itself is used as a food product, or as nutritional or dietary
CC   supplements, or in pharmaceutical compositions for lowering cholesterol.
CC   The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC   dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC   pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
CC   cookies, snack bars, confections, chocolates, and beverages. The
CC   alteration in sterol content and/or composition can also provide a plant
CC   with tolerance to stress and insect damage
XX
SQ   Sequence 356 BP; 98 A; 80 C; 78 G; 100 T; 0 U; 0 Other;

  Query Match             6.6%;  Score 109;  DB 5;  Length 356;
  Best Local Similarity   76.1%;  Pred. No. 1.8e-23;
  Matches  150;  Conservative    0;  Mismatches   40;  Indels    7;  Gaps    1;

Qy        338 GTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAA-------CAGGTCCTCTTTCT 390
              ||||||| || || |||||  |||| || ||||| ||||        |||||||||| |||
Db          1 GTCTTTCTGCAATTACAGAGCTGGACCCTGGTTATATAACAGGTTTCAGGTCCTCTCTCT 60

Qy        391 ACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATT 450
              | || |||||||| ||| | || |||||||| |||||||| || ||||| |||||||||
Db         61 TCAGTATGGAAAGAATGGGTCAAATGGTGTGTAGAGTTTGGCATTGAAGCTAATGCAATT 120

Qy        451 GTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTAC 510
              |||||||||| || ||||||||| || | ||| | |   | || ||| | || || |||
Db        121 ATCGCTGTTCCGTATGATTGGAGACTGCCCCCATCAATGCTTGAGGAGAGAGATCTGTAC 180

Qy        511 TTTCACAAGCTCAAGTT 527
              ||||||||  | |||||
Db        181 TTTCACAAATTAAAGTT 197


RESULT 9
ADF47831
ID   ADF47831 standard; DNA; 1872 BP.
XX
AC   ADF47831;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Schizosaccharomyces pombe acyltransferase DNA sequence SEQ ID NO:16.
XX
KW   acyltransferase; enzyme; membrane-spanning region;
KW   active membrane independent acyltransferase; fatty acid ester;
KW   fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW   phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW   acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
XX
OS   Schizosaccharomyces pombe.
XX
PN   WO2003100044-A1.
XX
PD   04-DEC-2003.
XX
PF   28-MAY-2003; 2003WO-SE000870.
XX
PR   29-MAY-2002; 2002SE-00001581.
PR   29-MAY-2002; 2002US-0383889P.
PR   20-JAN-2003; 2003SE-00000142.
XX
PA   (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI   Dahlqvist A,  Ghosal A,  Lindqvist Y,  Banas A;
XX
DR   WPI; 2004-053268/05.
DR   P-PSDB; ADF47832.
XX
PT   New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT   useful for producing structured lipids or fat-soluble molecules, in
PT   removing undesirable fat or in modifying lipids in animal or plant raw
PT   material.
XX
PS   Claim 5; SEQ ID NO 16; 91pp; English.
XX
CC   The present invention describes a nucleotide sequence (I) derived from a
CC   nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC   least one membrane-spanning region. (I) encodes an improved active
CC   membrane independent acyltransferase polypeptide in which at least one
CC   amino acid residue of the membrane-spanning region has been deleted
CC   and/or substituted as compared to the original acyltransferase
CC   polypeptide, where the encoded active membrane independent
CC   acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC   acid thioesters such as triacylglycerols, diacylglycerols,
CC   monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
```

CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC ; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridising to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 1872 BP; 598 A; 297 C; 405 G; 572 T; 0 U; 0 Other;

Query Match 3.2%; Score 52.6; DB 12; Length 1872;
Best Local Similarity 47.4%; Pred. No. 3.6e-05;
Matches 157; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

```
Qy        420 TGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTC 479
              || ||   |||||   ||  | |||   ||  |   || | | |||||||||| | || ||
Db        714 TGCTGCAATTGGTTATGAGCCTAATAACATGTTAAGTGCTTCTTACGATTGGCGGTTATC 773

Qy        480 ACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAAC 539
              |    | || || || || |||||    || |||   ||| | ||  ||  | ||||
Db        774 ATATGCAAATTTAGAGGAACGTGATAAATATTTTTCAAAGTTAAAAATGTTCATTGAGTA 833

Qy        540 TGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGT 599
                  |   | | |           |  |  || | || || ||||||    | ||
Db        834 CAGCAACATTGTACATAAGAAAAAGGTAGTGTTGATTTCTCACTCCATGGGTTCACAGGT 893

Qy        600 CTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTG 659
                  || ||| |  | ||| |       ||          |||   |     ||  ||
Db        894 TACGTACTATTTTTTTAAGTGGGTTGAAGCTGAGGGCTACGGAAATGGTGGACCGACTTG 953

Qy        660 GCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGA 719
              | || || | |||||  | || | | |  | |   |   || |  |||| |     |
Db        954 GGTTAATGATCATATTGAAGCATTTATAAATATATCGGGATCTTTGATTGGAGCACCCAA 1013

Qy        720 GGCAATCAAATCTACTCTCTCTGGTGTAACG 750
                || |   | |   | | || |||| || |
Db       1014 AACAGTGGCAGCGCTTTTATCGGGTGAAATG 1044
```

RESULT 10
ADF47817
ID ADF47817 standard; DNA; 1701 BP.
XX
AC ADF47817;
XX
DT 26-FEB-2004 (first entry)
XX
DE Yeast membrane independent acyltransferase DNA sequence SEQ ID NO:2.
XX
KW acyltransferase; enzyme; membrane-spanning region;
KW active membrane independent acyltransferase; fatty acid ester;
KW fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW acylated amino acid; structured lipid; fat-soluble molecule; yeast; gene;
KW ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2003100044-A1.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-SE000870.
XX
PR 29-MAY-2002; 2002SE-00001581.
PR 29-MAY-2002; 2002US-0383889P.
PR 20-JAN-2003; 2003SE-00000142.
XX
PA (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;
XX
DR WPI; 2004-053268/05.
XX
PT New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT useful for producing structured lipids or fat-soluble molecules, in
PT removing undesirable fat or in modifying lipids in animal or plant raw
PT material.
XX
PS Claim 12; SEQ ID NO 2; 91pp; English.
XX
CC The present invention describes a nucleotide sequence (I) derived from a
CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC least one membrane-spanning region. (I) encodes an improved active
CC membrane independent acyltransferase polypeptide in which at least one
CC amino acid residue of the membrane-spanning region has been deleted
CC and/or substituted as compared to the original acyltransferase
CC polypeptide, where the encoded active membrane independent
CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC acid thioesters such as triacylglycerols, diacylglycerols,
CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC ; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridising to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 1701 BP; 516 A; 317 C; 401 G; 467 T; 0 U; 0 Other;

Query Match 3.0%; Score 49.4; DB 12; Length 1701;
Best Local Similarity 49.2%; Pred. No. 0.00035;
Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

```
Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        530 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 589

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              | | |||   || ||    ||||||   ||||| |||       | |||      |
Db        590 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 649

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |       |    || |||  ||||| ||||||  | | |  ||   |
Db        650 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 709

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              ||||| || ||||| |   |   |||     | |         ||   |  |      |||
Db        710 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 769

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
```

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                || |  | || ||  || | |   |   ||  | ||   | ||||| ||  ||    |||
Db        770 TTAACGAACACATAGATTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 829

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              || |   | ||    |   ||||| || |
Db        830 CAGTTCCAGCTCTAATTAGTGGTGAAATG 858


RESULT 11
AAC64431
ID   AAC64431 standard; DNA; 1986 BP.
XX
AC   AAC64431;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Saccharomyces cerevisiae PDAT gene SEQ ID NO:1.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
DR   P-PSDB; AAB24256.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 45-48; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence encodes yeast (Saccharomyces
CC   cerevisiae) PDAT
XX
SQ   Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

  Query Match             3.0%;  Score 49.4;  DB 3;  Length 1986;
  Best Local Similarity   49.2%;  Pred. No. 0.00039;
  Matches  162;  Conservative    0;  Mismatches  161;  Indels    6;  Gaps    1;

Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        815 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 874

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              |  | |||   || ||    ||||||   ||||| |||       | |||     |
Db        875 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 934

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |        |    || |||  ||||| ||||||  | |  |  ||   |
Db        935 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 994

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              ||||| || ||||| |   |   |||     | |         ||   |  |       |||
Db        995 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 1054

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              || |  | || ||  || | |   |   ||  | ||   | ||||| ||  ||    |||
Db       1055 TTAACGAACACATAGATTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 1114

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              || |   | ||    |   ||||| || |
Db       1115 CAGTTCCAGCTCTAATTAGTGGTGAAATG 1143


RESULT 12
AAC64441
ID   AAC64441 standard; DNA; 1986 BP.
XX
AC   AAC64441;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Saccharomyces cerevisiae PDAT gene SEQ ID NO:1b.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
DR   P-PSDB; AAB24266.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 77-81; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the yeast
CC   (Saccharomyces cerevisiae) PDAT gene
XX
SQ   Sequence 1986 BP; 613 A; 366 C; 479 G; 528 T; 0 U; 0 Other;

  Query Match             3.0%;  Score 49.4;  DB 3;  Length 1986;
  Best Local Similarity   49.2%;  Pred. No. 0.00039;
  Matches  162;  Conservative    0;  Mismatches  161;  Indels    6;  Gaps    1;
```

```
Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        815 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 874

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              |  | |||   || ||    ||||||  |||||  |||       | |||     |
Db        875 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 934

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |       |    || |||  ||||| ||||||  | |  |  ||   |
Db        935 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 994

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              ||||| || |||||  |   |  |||    | |       ||   |  |      |||
Db        995 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 1054

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              || |  | || ||  |  | |   |  || | ||   | ||||| ||  ||   |||
Db       1055 TTAACGAACACATAGACTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 1114

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              || |   | ||   ||   ||||| || |
Db       1115 CAGTTCCAGCTCTACTTAGTGGTGAAATG 1143
```

RESULT 13
AAC64440
ID AAC64440 standard; DNA; 1986 BP.
XX
AC AAC64440;
XX
DT 12-FEB-2001 (first entry)
XX
DE Saccharomyces cerevisiae PDAT ORF nucleotide sequence SEQ ID NO:4a.
XX
KW PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200060095-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-EP002701.
XX
PR 01-APR-1999; 99EP-00106656.
PR 10-JUN-1999; 99EP-00111321.
PR 07-FEB-2000; 2000US-0180687P.
XX
PA (BADI) BASF PLANT SCI GMBH.
XX
PI Dahlqvist A, Stahl U, Lenman M, Banas A, Ronne H, Stymne S;
XX
DR WPI; 2000-665012/64.
DR P-PSDB; AAB24265.
XX
PT Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT pathway for triacylglycerol production and DNAs encoding them, useful for
PT producing triacylglycerol, or for transforming any cell or organism to
PT increase oil content.
XX
PS Claim 6; Page 71-74; 97pp; English.
XX
CC The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC independent reaction) the transfer of fatty acids from phospholipids to
CC diacylglycerol in the biosynthetic pathway for the production of
CC triacylglycerol (TAG). The enzyme is designated as
CC phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC nucleotides encoding them are useful for producing TAG and/or TAG with
CC uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC transforming any cell or organism in order to be expressed in this cell
CC or organism and result in an altered, preferably increased oil content of
CC this cell or organism. The present sequence represents the yeast
CC (Saccharomyces cerevisiae) PDAT ORF (open reading frame) nucleotide
CC sequence
XX
SQ Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Query Match 3.0%; Score 49.4; DB 3; Length 1986;
Best Local Similarity 49.2%; Pred. No. 0.00039;
Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

```
Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        815 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 874

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              |  | |||   || ||    ||||||  |||||  |||       | |||     |
Db        875 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 934

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |       |    || |||  ||||| ||||||  | |  |  ||   |
Db        935 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 994

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              |||||  || |||||  |   |  |||    | |       ||   |  |      |||
Db        995 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 1054

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              || |  | || ||  || | |   |  || | ||   | ||||| ||  ||   |||
Db       1055 TTAACGAACACATAGATTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 1114

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              || |   | ||   |   ||||| || |
Db       1115 CAGTTCCAGCTCTAATTAGTGGTGAAATG 1143
```

RESULT 14
AAS01342
ID AAS01342 standard; DNA; 1986 BP.
XX
AC AAS01342;
XX
DT 31-MAY-2001 (first entry)
XX
DE Yeast LCAT related open reading frame 1 (LRO1) gene.
XX
KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW nutritional supplement; dairy product; food product; salad dressing;
KW yeast; Arabidopsis thaliana; LCAT related open reading frame 1; LRO1; ds.
XX
OS Saccharomyces cerevisiae.
XX
FH Key Location/Qualifiers
FT CDS 1. .1986
FT /*tag= a
FT /product= "LRO1"
XX
PN WO200116308-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023863.
XX
PR 30-AUG-1999; 99US-0152493P.
XX
PA (MONS) MONSANTO CO.
XX
PI Lassner M, Van Eenennaam A;
XX
DR WPI; 2001-169010/17.
DR P-PSDB; AAU00464.
XX

PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT -like polypeptides, for modifying the sterol content and oil production
PT of plants.
XX
PS Claim 5; Page 116-117; 127pp; English.
XX
CC The present sequence encoding for yeast LCAT related open reading frame,
CC (LRO1) is described in an invention relating to several novel
CC polynucleotides encoding the plant sterol acyltransferases LCAT
CC (lecithin:cholesterol acyltransferase-like; AAS001081-AAS01104, AAS01341)
CC and ACAT (acyl CoA:cholesterol acyltransferase-like; AAS01311-AAS01319).
CC A rat ACAT-like cDNA sequence (AAS01105) is also described. The
CC polynucleotides encoding LCAT or ACAT are used to produce LCAT or ACAT
CC polypeptides. They can also be used in a recombinant construct to
CC transform a host cell (preferably of a plant) or a plant. The recombinant
CC construct is used to increase or decrease the sterol content of the host
CC cell or plant. It can be used to alter oil production of the cell or
CC plant, preferably by increasing it. The oil of the plant or the plant
CC itself is used as a food product, or as nutritional or dietary
CC supplements, or in pharmaceutical compositions for lowering cholesterol.
CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
CC cookies, snack bars, confections, chocolates, and beverages. The
CC alteration in sterol content and/or composition can also provide a plant
CC with tolerance to stress and insect damage
XX
SQ Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Query Match 3.0%; Score 49.4; DB 5; Length 1986;
Best Local Similarity 49.2%; Pred. No. 0.00039;
Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

```
Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        815 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 874

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              |  | |||   || ||    ||||||   ||||| |||        | |||     |
Db        875 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 934

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |        |    || |||  ||||| ||||||  | |  |  ||   |
Db        935 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 994

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              |||||  || |||||  |    |   |||    | |        ||   |  |      |||
Db        995 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 1054

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              || |  | || ||  || | |   |   ||  | ||   | |||||  ||  ||    |||
Db       1055 TTAACGAACACATAGATTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 1114

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              ||  |   | ||    |   ||||| || |
Db       1115 CAGTTCCAGCTCTAATTAGTGGTGAAATG 1143
```

RESULT 15
ADF47816
ID ADF47816 standard; DNA; 1986 BP.
XX
AC ADF47816;
XX
DT 26-FEB-2004 (first entry)
XX
DE Yeast acyltransferase nucleotide sequence SEQ ID NO:1.
XX
KW acyltransferase; enzyme; membrane-spanning region;
KW active membrane independent acyltransferase; fatty acid ester;
KW fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW acylated amino acid; structured lipid; fat-soluble molecule; yeast; gene;
KW ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2003100044-A1.
XX
PD 04-DEC-2003.
XX
PF 28-MAY-2003; 2003WO-SE000870.
XX
PR 29-MAY-2002; 2002SE-00001581.
PR 29-MAY-2002; 2002US-0383889P.
PR 20-JAN-2003; 2003SE-00000142.
XX
PA (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI Dahlqvist A, Ghosal A, Lindqvist Y, Banas A;
XX
DR WPI; 2004-053268/05.
DR P-PSDB; ADF47818.
XX
PT New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT useful for producing structured lipids or fat-soluble molecules, in
PT removing undesirable fat or in modifying lipids in animal or plant raw
PT material.
XX
PS Claim 5; SEQ ID NO 1; 91pp; English.
XX
CC The present invention describes a nucleotide sequence (I) derived from a
CC nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC least one membrane-spanning region. (I) encodes an improved active
CC membrane independent acyltransferase polypeptide in which at least one
CC amino acid residue of the membrane-spanning region has been deleted
CC and/or substituted as compared to the original acyltransferase
CC polypeptide, where the encoded active membrane independent
CC acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC acid thioesters such as triacylglycerols, diacylglycerols,
CC monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
CC acylated carbohydrates and acylated amino acids. Also described: (1) a
CC nucleotide sequence molecule (II) comprising at least one promoter region
CC which functions in a host, where the promoter region is operably linked
CC to at least one (I), which is operably linked to at least one non-
CC translated region which functions in a host; (2) a vector comprising (II)
CC ; (3) a host cell comprising (II) or the vector; (4) producing an
CC improved active membrane independent acyltransferase polypeptide,
CC comprising providing the above host cell and a growth medium preparing a
CC host cell culture, culturing the host cell culture and harvesting the
CC host cell culture and recovering the improved active membrane independent
CC acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC (4), where the polypeptide at least is an improved active membrane
CC independent acyltransferase polypeptide; (6) an oligonucleotide
CC specifically hybridising to (I) under stringent conditions; and (7) a kit
CC comprising the above polypeptide and a stabiliser. The nucleic acid
CC molecule (I) and the polypeptide are useful in producing structured
CC lipids or fat-soluble molecules, in removing undesirable fat or in
CC modifying lipids present in animal and plant raw material. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 1986 BP; 615 A; 361 C; 478 G; 532 T; 0 U; 0 Other;

Query Match 3.0%; Score 49.4; DB 12; Length 1986;
Best Local Similarity 49.2%; Pred. No. 0.00039;
Matches 162; Conservative 0; Mismatches 161; Indels 6; Gaps 1;

```
Qy        428 TTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCA 487
              ||||    ||| | |||  |||      || | | || ||||||||  |  ||
Db        815 TTGGCTATGAACCCAATAAAATGACGAGTGCTGCGTATGATTGGAGGCTTGCATATTTAG 874

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              |  | |||   || ||    ||||||   ||||| |||        | |||     |
Db        875 ATCTAGAAAGACGCGATAGGTACTTTACGAAGCTAAAGGAACAAATCGAACTGTTTCATC 934
```

```
Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              || |  |||| |       |    || |||  ||||| ||||||  | |  |  ||   |
Db        935 AATTGAGTGGTGAAAAAGTTTGTTTAATTGGACATTCTATGGGTTCTCAGATTATCTTTT 994

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCA------AAACATTATTTGAAGTGGC 661
              ||||| || |||||  |   |   |||    | |         ||   |  |      |||
Db        995 ACTTTATGAAATGGGTCGAGGCTGAAGGCCCTCTTTACGGTAATGGTGGTCGTGGCTGGG 1054

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              || |  | || ||  || | |   |   ||  | ||   | |||| ||  ||    |||
Db       1055 TTAACGAACACATAGATTCATTCATTAATGCAGCAGGGACGCTTCTGGGCGCTCCAAAGG 1114

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACG 750
              || |   | ||    |   ||||| || |
Db       1115 CAGTTCCAGCTCTAATTAGTGGTGAAATG 1143
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Search completed: November 8, 2004, 22:55:43
Job time : 840 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:37:51 ; Search time 5402 Seconds
(without alignments)
11069.530 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgaattcgaaatc.....ttgataaaagtgggtattaa 1641

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	484	29.5	596	1	AU237072	AU237072
2	464.2	28.3	946	7	CK259394	CK259394 EST705472
3	438.8	26.7	752	7	CF844688	CF844688 psHB029xF
4	397	24.2	713	7	CK939714	CK939714 CGF100474
5	386.2	23.5	788	7	CK259393	CK259393 EST705471
6	376.8	23.0	968	7	CK260764	CK260764 EST706842
7	374.8	22.8	686	5	BQ508623	BQ508623 EST616038
8	367	22.4	792	4	BG600021	BG600021 EST504916
9	350.8	21.4	565	5	BQ584361	BQ584361 E011859-0
10	343	20.9	560	6	CD710878	CD710878 VVA026C02
11	331.8	20.2	676	6	CA090564	CA090564 SCSGAM210
12	316.4	19.3	534	1	AI974291	AI974291 T110293e
13	306.6	18.7	628	4	BI267124	BI267124 NF097C07I
14	293.4	17.9	728	1	AU306500	AU306500 AU306500
15	291.8	17.8	683	6	CA221313	CA221313 SCSGFL403
16	268.8	16.4	647	6	CA156623	CA156623 SCEPRZ308
17	226.6	13.8	502	7	CK115712	CK115712 Y014D01 P
18	208.6	12.7	394	1	AU290926	AU290926 AU290926
19	207.6	12.7	704	4	BI422757	BI422757 EST533423
20	206.2	12.6	488	4	BI267156	BI267156 NF101G04I
21	189.2	11.5	792	4	BG367066	BG367066 HVSMEi001
22	185	11.3	632	4	BI922233	BI922233 EST542136
23	182.2	11.1	559	2	AW760400	AW760400 sl49g03.y
24	180.4	11.0	518	2	BE321377	BE321377 NF042H09I
25	176.8	10.8	666	8	BH974706	BH974706 odj06g04.
c 26	168.6	10.3	698	7	CO532456	CO532456 3530_1_21
27	167.6	10.2	1225	8	B11175	B11175 F14L4-Sp6 I
28	165.6	10.1	625	8	BH944186	BH944186 obu90a02.
c 29	160.2	9.8	692	7	CO521704	CO521704 3530_1_14
c 30	160	9.8	542	2	AW120335	AW120335 614089B09
c 31	159	9.7	840	7	CK260765	CK260765 EST706843
32	137	8.3	582	1	AU287072	AU287072 AU287072
33	135.2	8.2	207	8	BH746163	BH746163 qo78e11.b
34	134.8	8.2	503	4	BI595853	BI595853 949023G05
c 35	133.4	8.1	303	8	BH548609	BH548609 BOHCO62TF
36	133.4	8.1	737	1	AJ611569	AJ611569 AJ611569
c 37	126.6	7.7	493	9	CC948076	CC948076 BOIHF12TF
38	123.8	7.5	546	9	CC948085	CC948085 BOIHF12TR
39	122.4	7.5	486	1	AI771341	AI771341 EST252441
40	122.4	7.5	496	1	AI488511	AI488511 EST246850
41	122.4	7.5	709	1	AI486635	AI486635 EST244956
42	118.6	7.2	429	1	AI488359	AI488359 EST246681
43	113.2	6.9	967	8	CC373126	CC373126 PUHBZ32TB
44	106.2	6.5	579	7	CO722489	CO722489 Mdfr3017i
45	104.8	6.4	712	4	BI932257	BI932257 EST552146

ALIGNMENTS

RESULT 1
AU237072
LOCUS AU237072 596 bp mRNA linear EST 01-APR-2002
DEFINITION AU237072 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-47-A08 5', mRNA sequence.
ACCESSION AU237072
VERSION AU237072.1 GI:19876241
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 596)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
FEATURES Location/Qualifiers
source 1. .596
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-47-A08"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"
ORIGIN

Query Match 29.5%; Score 484; DB 1; Length 596;

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  Best Local Similarity   99.4%;  Pred. No. 9.9e-134;
  Matches  484;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 169

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 229

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 289

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 349

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 409

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 469

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        470 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTNAAGTGGTGT 529

Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
              |||||||||||| |||||||||||||||||||||||||||||||||||||||| ||||
Db        530 GTTGAGTTTGGTNTAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATNGTCA 589

Qy        481 CCAACCA 487
              |||||||
Db        590 CCAACCA 596


RESULT 2
CK259394
LOCUS       CK259394                946 bp    mRNA    linear   EST 03-AUG-2004
DEFINITION  EST705472 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAB029 5' end, mRNA sequence.
ACCESSION   CK259394
VERSION     CK259394.1  GI:39816372
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 946)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST705470 EST705471 EST705473
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from the University of Arizona Genomics
            Institute via http://genome.arizona.edu/orders/ .
            Seq primer: CAG GAA ACA GCT ATG ACC.
FEATURES             Location/Qualifiers
     source          1. .946
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POAB029"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."
ORIGIN

  Query Match           28.3%;  Score 464.2;  DB 7;  Length 946;
  Best Local Similarity   70.7%;  Pred. No. 1.1e-127;
  Matches  671;  Conservative    0;  Mismatches  253;  Indels   25;  Gaps    3;

Qy        678 TGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCT 737
              ||| ||||| |||||||||||||||||||||||| || | ||| || ||||| | ||  |
Db          1 TGCCTATTTTGCTGTTGGAGCTCCTCTTCTTGGTGCTATCGAGACAGTCAAAGCAACATT 60

Qy        738 CTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTC 797
              || ||    || |||||| |||||||||||| ||||| || |||||  || ||| |||| |
Db         61 ATCGGGGTCTACATTTGGTCTTCCTGTTTCAGAGGGGACAGCTCGCCTGATGTTCAATAC 120

Qy        798 TTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGGGTGATAACACATC 857
              ||||  || ||  | ||| |  | |||||||||||  |||| |    ||||||  |||
Db        121 ATTTGGATCTTCTATATGGATGTTACCATTTTCAAAATATTGTACAACTGATAATGCATA 180

Qy        858 CTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATGA 917
              |||  ||||| |||   ||||      |  ||| |  | |  |  |||||| || |||||
Db        181 TCGGAGACATTTCTCT---GGTGGAAACAGAAAATACCATCATGCCTACCATTGCGATGA 237

Qy        918 AGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTCC 977
              | |||  | ||||||| || |||||||||| ||||| || || || |||||| ||||
Db        238 GCATGAACTTAAATCAAAGTACTCTGGCTGGCCAACAAACATAATCAATATTGAAGTTCC 297

Qy        978 TTCCACTAG--------------------CGTTACAGAAACAGCTCTAGTCAACATGAC 1016
              ||| | | |                    |||  |||||| || | |  |||| || |
Db        298 TTCGATTCGAGGGAATGAGGTTTATCCCTCAGTTGTAGAAACTGCCCAAACCAACTTGTC 357

Qy       1017 CAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGG 1076
              | |||||||||||  | || || |  ||||| ||  | || |||||| |  | || ||
Db        358 TGGAATGGAATGTGGATTCCCGACACAATTGTCCTTTTCTGCTCGTGAAGTCTCTGACGG 417

Qy       1077 GACTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTT 1136
              ||  |||||||||| ||| |  | ||||| || || ||  | ||  | || ||||  ||
Db        418 AACCTTTTTCAAAGCCATAAAGAATTATGATCCTGACAGTGAAAGACTCTTTCACCTTTT 477

Qy       1137 AAAGAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACC 1196
              ||| ||||  || |||||||| ||  |||| |||||||| || |||||||| ||||||||
Db        478 AAAAAAGTCTTACCATGATGATCCGATTTTAAATCCTCTAACACCTTGGGAAAGACCACC 537

Qy       1197 TATAAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTT 1256
              | | || ||  |||| ||||| ||||| |   ||   ||||| ||||||||||| || ||
Db        538 TCTCAAGAACATATTCTGCATTTATGGCGTAGATTCGAAGACTGAGGTTGGTTACTATTT 597

Qy       1257 TGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAAC 1316
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Db        598 TGCACCAAGTGGGAAGCCTTATCCTGATAATTGGATTATAACAGATGTGATATATGAAAT 657

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Db        658 CGAAGGATCTCTGTATTCCCGGTCAGGAAATCTGGTTGAAGGAAACCCTGGTGCAACAAG 717

Qy       1377 TGGGGATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAA 1436

Db        718 TGGGGATGAGACGGTGCCATACCATTCCCTCTCCTGGTGCAAGAATTGGCTGGGGCCAAA 777

Qy       1437 AGTTAACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACT 1496

Db        778 AGTGAACATAACAAGGACACCACAGTCAGAGCATGATGGCTCAGCTGTACAAGTGCATCA 837

Qy       1497 AAATGTTGATCAT-GAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGG 1555

Db        838 AAATATAGAGCATCCAACATGGTGAAGATATCATTCCCAATATGACAAAGTTAGCTACAA 897

Qy       1556 TTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAG 1604

Db        898 TGAAGTACATAACCTATTATGAGGATTCTGAAAGTTTTCCAGGAACGAG 946


RESULT 3
CF844688
LOCUS       CF844688                752 bp    mRNA    linear   EST 30-OCT-2003
DEFINITION  psHB029xF13f USDA-IFAFS:Expression of Phytophthora sojae genes
            during infection and propagation_sHB Phytophthora sojae cDNA clone
            sHB029F13 5, mRNA sequence.
ACCESSION   CF844688
VERSION     CF844688.1  GI:38060342
KEYWORDS    EST.
SOURCE      Phytophthora sojae
  ORGANISM  Phytophthora sojae
            Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
            Phytophthora.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Tyler,B.
  TITLE     Tyler,B. Not Published
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Tyler B
            Tyler lab
            VBI
            1880 Pratt Dr., Blacksburg, VA 24061, USA
            Tel: 540-231-7318
            Email: bmtyler@vt.edu
            PCR PRimers
            FORWARD: BK reverse primer
            BACKWARD: BK reverse primer
            Plate: 029  row: F  column: 13
            Seq primer: BK reverse primer
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Phytophthora sojae"
                     /mol_type="mRNA"
                     /db_xref="taxon:67593"
                     /clone="sHB029F13"
                     /tissue_type="mycelium"
                     /cell_line="P6497"
                     /dev_stage="48 hr. post infection stage"
                     /lab_host="Soybean plant"
                     /clone_lib="USDA-IFAFS:Expression of Phytophthora sojae
                     genes during infection and propagation_sHB"
                     /note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
ORIGIN

  Query Match             26.7%;  Score 438.8;  DB 7;  Length 752;
  Best Local Similarity   79.9%;  Pred. No. 4.4e-120;
  Matches  526;  Conservative    0;  Mismatches  131;  Indels    1;  Gaps    1;

Qy        108 CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGC 167

Db         94 CGACTACTCGAAGCTCTCCGGCATTATAATCCCTGGCTTCGCATCCACTCAGCTCCGAGC 153

Qy        168 GTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATG 227

Db        154 ATGGTCCATTCTCGACTGTCCTTACTCTCCGCTCGATTTCAACCCTCTCGATTTGGTCTG 213

Qy        228 GCTAGACACCACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGA 287

Db        214 GCTCGACACAACCAAACTTCTTTCTGCTGTCAATTGCTGGCTTAAGTGTATGGTGTTGGA 273

Qy        288 TCCTTATAATCAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGC 347

Db        274 TCCTTACAATCAGACAGATCATCCTGATTGCAAGTCCCGTCCTGATAGTGGTCTTTCTGG 333

Qy        348 CATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTG 407

Db        334 TATTACAGAACTTGATCCGGGTTATATAACAGGACCTCTTTCATCGGTTTGGAAAGAATG 393

Qy        408 GCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGA 467

Db        394 GATTAAGTGGTGTATTGAATTTGGCATAGAAGCTAATGCAATAATTGCTGTTCCATATGA 453

Qy        468 TTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTT 527

Db        454 TTGGAGATTGTCGCCCTCCAAGCTTGAAGAGCGGGACCTTTACTTTCATAAGCTAAAAAT 513

Qy        528 GACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAAT 587

Db        514 AACATTTGAAACTGCTTACAAACTTCGTGGTGGCCCCTCTTTAGTTTTTGCCCATTCATT 573

Qy        588 GGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACA 647

Db        574 GGGTAATCATGTTTTCCGTTATTTCTTGGAGTGGTTGAAGCTAGAGATTGCACCANAACA 633

Qy        648 TTATTTGAAGTGGCTT-GATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTC 706

Db        634 TTATATCCAGTGGGTTGGATCAACATATTCGTGCCTATNTTGCTGTTGGAGCTCCCCTTC 693

Qy        707 TTGGTTCTGTTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGT 764

Db        694 TTGGTGCANTGGANACCATTGAAGCAACACTTTCTGGATTCACATTTGGTCTTCCTAT 751


RESULT 4
CK939714
LOCUS       CK939714                713 bp    mRNA    linear   EST 19-MAR-2004
DEFINITION  CGF1004746_F04 Developing fruit flavedo at 165 DAFB Citrus sinensis
            cDNA clone F1650002_IIF_F04 5', mRNA sequence.
ACCESSION   CK939714
VERSION     CK939714.1  GI:45452970
KEYWORDS    EST.
SOURCE      Citrus sinensis
  ORGANISM  Citrus sinensis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE   1  (bases 1 to 713)
  AUTHORS   Uratsu,S., Baek,J., Leslie,A., Xu,J., Cook,D. and Dandekar,A.
  TITLE     Analysis of peel specific genes in Citrus (2004)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Abhaya Dandekar, PhD
            CAES Genome Facility
            UC Davis, Department of Pomology
            One Shields Ave, Davis, CA 95616, USA
            Tel: 530 752 7784
            Fax: 530 752 8502
            Email: amdandekar@ucdavis.edu
            Seq primer: WSC-F-TCCGAGATCTGGACGAGC.
FEATURES             Location/Qualifiers
     source          1. .713
                     /organism="Citrus sinensis"
                     /mol_type="mRNA"
                     /cultivar="Washington navel orange"
```

/db_xref="taxon:2711"
/clone="F1650002_IIF_F04"
/sex="Hermaphrodite"
/cell_type="Falvedo"
/dev_stage="Developing fruit sample-collected October 22, 2003"
/lab_host="XL10-Gold"
/clone_lib="Developing fruit flavedo at 165 DAFB"
/note="Organ: Fruit; Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; Developing citrus fruits were harvested from trees growing in the 'Citrus variety collection' in the Wolfskill experimental orchard located in Winters, California (USA). Fruit was collected on October 22, 2003, between 8 to 9 am and stored at 4C. The flavedo tissue was dissected out of developing fruit (165 DAFB) and used to isolate RNA using Trizol reagent from Invitrogen. The cDNA Library was constructed using the SMART cDNA library Kit (Clontech). The primary library was en masse evicted and plasmid DNA containing the cDNA library was isolated from the resultant bacterial population. Plasmid DNA was then transformed into ultra competent E coli cells (XL10 Gold; Stratagene). Transformants were plated out on Q-trays (2000 cfu/tray), picked using a Qbot and archived in 384 well dishes."

ORIGIN

Query Match 24.2%; Score 397; DB 7; Length 713;
Best Local Similarity 76.9%; Pred. No. 1.6e-107;
Matches 484; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

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Qy         28 GCTTCCTTCACCGTCATCGCCGTTTTTTTCTTGATTTGCGGTGGCCGAACTGCGGTGGAG 87
              |||  | ||  | || ||| |||  |  |  || || | |     ||    ||    | |
Db         84 GCTGTCGTCCTCCTCCTCGTCGTCGTCGTTCTGCTTGGAGCCCTGCGCGAAGCCTCCGCG 143

Qy         88 GATGAGACCGAGTTTCACGGCGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTT 147
                | |    ||||||   ||| |||||| | ||| | || || || || || || || ||| |||
Db        144 AAAGGCGGCGAGTTCACCGGGGACTACCCCAAGTTGTCCGGAATCATAATACCAGGCTTT 203

Qy        148 GCGTCGACGCAGCTACGAGCGTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTC 207
              |||||||| |||||  |||| |||||  |||||  |||||||| ||| ||||   | || |||
Db        204 GCGTCGACTCAGCTGAGAGCATGGTCAATCCTCGACTGTCCGTACTCTCCTCTCGATTTC 263

Qy        208 AATCCGCTCGACCTCGTATGGCTAGACACCACTAAGCTTCTTTCTGCTGTCAACTGCTGG 267
              || || ||||||||||| |||||||||| || || |||||||||||||| ||||| |||
Db        264 AACCCTCTCGACCTCGTCTGGCTAGACACTACCAAACTTCTTTCTGCTGTGAACTGTTGG 323

Qy        268 TTTAAGTGTATGGTGCTAGATCCTTATAATCAAACAGACCATCCCGAGTGTAAGTCACGG 327
              |||||||  |||   |||||||||| ||||||||||  |||||||  || |||||  ||
Db        324 CTTAAGTGCATGACACTAGATCCTTACAATCAAACAGATAATCCCGAATGCAAGTCTCGA 383

Qy        328 CCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTT 387
              |||||  |||||||||||  ||  ||  ||||||  |  ||||||||||  ||||||||||||||
Db        384 CCTGATAGTGGTCTTTCCGCAATTACAGAACTTGATCCAGGTTATATAACAGGTCCTCTG 443

Qy        388 TCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCA 447
              ||  | ||  ||||||||  |||  ||||||||||  |||||||||||||||||  ||  |||  ||
Db        444 TCCTCAGTGTGGAAAGAATGGGTTAAGTGGTGCGTTGAGTTTGGTATAGAGGCTAATTCA 503

Qy        448 ATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTT 507
              ||  | ||  | ||||||  |||||||||||||||||||  | ||  |  ||  |||  | ||||||
Db        504 ATCATTGCCGCTCCATATGATTGGAGATTGTCACCATCAAAGCTCGAGGAGAGAGACCTT 563

Qy        508 TACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCT 567
              ||  ||||||||  ||  ||||||||  ||||||||||  |  |||||  |||||  |||||  ||
Db        564 TATTTTCACAAACTAAAGTTGACATTTGAAACTGCCCTTAAACTTCGTGGTGGCCCCTCA 623

Qy        568 ATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGG 627
              ||||  ||||  ||||||  |||||||||||||  ||  |  ||||||||||  |||||  | |
Db        624 TTAGTTCTTGCTCATTCATTGGGTAATAATGTGTTTCGTTACTTTCTGGAGTGGCTAAAG 683

Qy        628 CTAGAAATTGCACCAAAACATTATTTGAA 656
              ||||||||  |  ||||||||  |||  |  ||
Db        684 TTAGAAATTCCCCCAAAACAATATATCAA 712
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RESULT 5
CK259393
LOCUS CK259393 788 bp mRNA linear EST 03-AUG-2004
DEFINITION EST705471 potato abiotic stress cDNA library Solanum tuberosum cDNA clone POAB029 5' end, mRNA sequence.
ACCESSION CK259393
VERSION CK259393.1 GI:39816371
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 788)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
TITLE Generation of ESTs from abiotic stressed potato tissue
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST705470 EST705472 EST705473
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/ .
Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES Location/Qualifiers
source 1. .788
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAB029"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots:3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 23.5%; Score 386.2; DB 7; Length 788;
Best Local Similarity 71.2%; Pred. No. 3e-104;
Matches 563; Conservative 0; Mismatches 203; Indels 25; Gaps 3;

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Qy        678 TGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCT 737
              ||| ||||| |||||||||||||||||||||||| || | ||| || ||||| | ||  |
Db          1 TGCCTATTTTGCTGTTGGAGCTCCTCTTCTTGGTGCTATCGAGACAGTCAAAGCAACATT 60

Qy        738 CTCTGGTGT-AACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATT 796
                 || || ||  || ||||| |||||||||| ||||| || |||||  || ||| ||||
Db         61 ATCCGGGGTCTACATTTGGTCTTCCTGTTTCAGAGGGGACAGCTCGCCTGATGTTCAATA 120
```

```
Qy        797 CTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGGGTGATAACACAT 856
              | ||||  || ||  | ||| |  | ||||||||||||  |||| |     ||||||  |||
Db        121 CATTTGGATCTTCTATATGGATGTTACCATTTTCAAAATATTGTACAACTGATAATGCAT 180

Qy        857 CCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATG 916
                |||  ||||| |||   ||||      |  ||| |  | |  |  ||||| || ||||
Db        181 ATCGGAGACATTTCTCT---GGTGGAAACAGAAAATACCATCATGCCTACCATTGCGATG 237

Qy        917 AAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTC 976
              |  | |||  | |||||||  || ||||||||||| |||||  || ||  ||  |||||| |||
Db        238 AGCATGAACTTAAATCAAAGTACTCTGGCTGGCCAACAAACATAATCAATATTGAAGTTC 297

Qy        977 CTTCCACTAG----------------------CGTTACAGAAACAGCTCTAGTCAACATGA 1015
              ||||  |  |  |                      |||  |||||  ||  |  |  ||||  ||
Db        298 CTTCGATTCGAGGGAATGAGGTTTATCCCTCAGTTGTAGAAACTGCCCAAACCAACTTGT 357

Qy       1016 CCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATG 1075
              |  | ||||||||||  |  || || |  |||||  ||  |  ||  |||||  |  |  || |
Db        358 CTGGAATGGAATGTGGATTCCCGACACAATTGTCCTTTTCTGCTCGTGAAGTCTCTGACG 417

Qy       1076 GGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGT 1135
              | ||  |||||||||| ||| |  | |||||  || || ||  |  |||  | ||  ||||   |
Db        418 GAACCTTTTTCAAAGCCATAAAGAATTATGATCCTGACAGTGAAAGACTCTTTCACCTTT 477

Qy       1136 TAAAGAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCAC 1195
              ||||  ||||   ||  |||||||| ||   |||| ||||||||  || ||||||||  |||||||
Db        478 TAAAAAAGTCTTACCATGATGATCCGATTTTAAATCCTCTAACACCTTGGGAAAGACCAC 537

Qy       1196 CTATAAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACT 1255
              || | ||  ||  |||| |||||  |||||  |    ||   |||||  ||||||||||  || |
Db        538 CTCTCAAGAACATATTCTGCATTTATGGCGTAGATTCGAAGACTGAGGTTGGTTACTATT 597

Qy       1256 TTGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAA 1315
              ||||  |||||||| || ||||||||||||||||||||| || || ||| | || || ||||
Db        598 TTGCACCAAGTGGGAAGCCTTATCCTGATAATTGGATTATAACAGATGTGATATATGAAA 657

Qy       1316 CTGAAGGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAA 1375
                |||||  ||  ||     ||  |||| |||| | |||||||  || |||  ||||   | | ||
Db        658 TCGAAGGATCTCTGTATTCCCGGTCAGGAAATCTGGTTGAAGGAAACCCTGGTGCAACAA 717

Qy       1376 CTGGGGATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTA 1435
              ||||||||||||||| || || ||||| ||||| |||||||||||||||||| || || |
Db        718 GTGGGGATGAGACGGTGCCATACCATTCCCTCTCCTGGTGCAAGAATTGGCTGGGGCCAA 777

Qy       1436 AAGTTAACATA 1446
              |||| ||||||
Db        778 AAGTGAACATA 788
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RESULT 6
CK260764
LOCUS       CK260764                968 bp    mRNA    linear   EST 03-AUG-2004
DEFINITION  EST706842 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAB552 5' end, mRNA sequence.
ACCESSION   CK260764
VERSION     CK260764.1  GI:39817742
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 968)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST706843
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from the University of Arizona Genomics
            Institute via http://genome.arizona.edu/orders/ .
            Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES             Location/Qualifiers
     source          1. .968
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POAB552"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."
ORIGIN
```

```
  Query Match             23.0%;  Score 376.8;  DB 7;  Length 968;
  Best Local Similarity   74.1%;  Pred. No. 2.2e-101;
  Matches  477;  Conservative    0;  Mismatches  167;  Indels    0;  Gaps    0;

Qy        988 GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTG 1047
              |||  ||||||  || | |  |||| || |  | ||||||||||  | || || |  |||
Db         22 GTTGTAGAAACTGCCCAAACCAACTTGTCTGGAATGGAATGTGGATTCCCGACACAATTG 81

Qy       1048 TCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGAC 1107
              ||  ||   | ||  |||||  |  | |||||  ||  ||||||||||  |||  |  | |||||
Db         82 TCCTTTTCTGCTCGTGAAGTCTCTGATGGAACCTTTTTCAAAGCCATAAAGAATTATGAT 141

Qy       1108 CCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTT 1167
              ||  ||  ||  |  ||  |  ||  ||||   |||||  ||||   ||  ||||||||  ||  ||||
Db        142 CCTGACAGTGAAAGACTCTTTCACCTTTTAAAAAAGTCTTACCATGATGATCCGATTTTA 201

Qy       1168 AATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCT 1227
              ||||||||  ||  ||||||||  |||||||||  |  ||  ||||  |||||  |||||  |
Db        202 AATCCTCTAACACCTTGGGAAAGACCACCTCTCAAGAACATATTCTGCATTTATGGCGTA 261

Qy       1228 CATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAAT 1287
                ||   |||||  ||||||||||  ||  |||||  ||||||||  ||  ||||||||||||||
Db        262 GATTCGAAGACTGAGGTTGGTTACTATTTTGCACCAAGTGGGAAGCCTTATCCTGATAAT 321

Qy       1288 TGGATCATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACT 1347
              |||||  ||  ||  |||  |  ||  ||  ||||   |||||  ||  ||     ||   ||||  |||| |
Db        322 TGGATTATAACAGATGTGATATATGAAATCGAAGGATCTCTGTATTCCCGGTCAGGAAAT 381

Qy       1348 GTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTC 1407
                |||||||  ||  |||  ||||   |  |  ||  ||||||||||||||||  ||  ||  |||||  |||
Db        382 CTGGTTGAAGGAAACCCTGGTGCAACAAGTGGGGATGAGACGGTGCCATACCATTCCCTC 441

Qy       1408 TCTTGGTGCAAGAATTGGCTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAA 1467
              ||  ||||||||||||||||  ||  ||  |||||  ||||||||||  |  |  ||  |||  ||||
Db        442 TCCTGGTGCAAGAATTGGCTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAG 501
```

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Qy       1468 CACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATC 1527
Db        502 CATGATGGCTCAGCTGTACAAGTGCATCAAAATATAGAGCATCAACATGGTGAAGATATC 561

Qy       1528 ATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAG 1587
Db        562 ATTCCCAATATGACAAAGTTAGCTACAATGAAGTACATAACCTATTATGAGGATTCTGAA 621

Qy       1588 AGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAAAG 1631
Db        622 AGTTTTCCAGGAACGAGAACAGCAGTTTGGGAGCTTGATAAAGG 665
```

RESULT 7
BQ508623
LOCUS BQ508623 686 bp mRNA linear EST 07-MAR-2003
DEFINITION EST616038 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMGX37 5' end, mRNA sequence.
ACCESSION BQ508623
VERSION BQ508623.2 GI:21924395
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 686)
AUTHORS Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and Karamycheva,S.A.
TITLE Generation of a set of potato cDNA clones for microarray analyses
JOURNAL Unpublished (2002)
COMMENT On Jun 10, 2002 this sequence version replaced gi:21367492.
Other_ESTs: EST616039
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .686
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMGX37"
/tissue_type="mixed tissues"
/lab_host="SOLR"
/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes, tubers, or roots."
ORIGIN

Query Match 22.8%; Score 374.8; DB 5; Length 686;
Best Local Similarity 74.0%; Pred. No. 7.6e-101;
Matches 475; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

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Qy        988 GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTG 1047
Db          4 GTTGTAGAAACTGCCCAAACCAACTTGTCTGGAATGGAATGTGGATTCCCGACACAATTG 63

Qy       1048 TCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGAC 1107
Db         64 TCCTTTTCTGCTCGTGAAGTCTCTGACGGAACCTTTTTCAAAGCCATAAAGAATTATGAT 123

Qy       1108 CCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTT 1167
Db        124 CCTGACAGTGAAAGACTCTTTCACCTTTTAAAAAAGTCTTACCATGATGATCCGATTTTA 183

Qy       1168 AATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCT 1227
Db        184 AATCCTCTAACACCTTGGGAAAGACCACCTCTCAAGAACATATTCTGCATTTATGGCGTA 243

Qy       1228 CATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAAT 1287
Db        244 GATTCGAAGACTGAGGTTGGTTACTATTTTGCACCAAGTGGGAAGCCTTATCCTGATAAT 303

Qy       1288 TGGATCATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACT 1347
Db        304 TGGATTATAACAGATGTGATATATGAAATCGAAGGATCTCTGTATTCCCGGTCAGGAAAT 363

Qy       1348 GTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTC 1407
Db        364 CTGGTTGAAGGAAACCCTGGTGCAACAAGTGGGGATGAGACGGTGCCATACCATTCCCTC 423

Qy       1408 TCTTGGTGCAAGAATTGGCTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAA 1467
Db        424 TCCTGGTGCAAGAATTGGCTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAG 483

Qy       1468 CACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATC 1527
Db        484 CATGATGGCTCAGCTGTACAAGTGCATCAAAATATAGAGCATCAACATGGTGGAGATATC 543

Qy       1528 ATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGAG 1587
Db        544 ATTCCCAATATGACAAAGTTAGCTACAATGAAGTACATAACCTATTATGAGGATTCTGAA 603

Qy       1588 AGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAA 1629
Db        604 AGTTTTCCAGGAACGAGAACAGCAGTTTGGGAGCTTGATAAA 645
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RESULT 8
BG600021
LOCUS BG600021 792 bp mRNA linear EST 07-MAR-2003
DEFINITION EST504916 cSTS Solanum tuberosum cDNA clone cSTS27C13 5' sequence, mRNA sequence.
ACCESSION BG600021
VERSION BG600021.1 GI:13617157
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 792)
AUTHORS van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
TITLE Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.
FEATURES Location/Qualifiers
source 1. .792
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS27C13"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"

/clone_lib="cSTS"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."

ORIGIN

Query Match 22.4%; Score 367; DB 4; Length 792;
Best Local Similarity 74.2%; Pred. No. 1.8e-98;
Matches 477; Conservative 0; Mismatches 165; Indels 1; Gaps 1;

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Qy       988 GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTG 1047
Db         4 GTTGTAGAAACTGCCCAAACCAACTTGTCTGGAATGGAATGTGGATTCCCGACACAATTG 63

Qy      1048 TCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGAC 1107
Db        64 TCCTTTTCTGCTCGTGAAGTCTCTGACGGAACCTTTTTCAAAGCCATAAAGAATTATGAT 123

Qy      1108 CCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTT 1167
Db       124 CCTGACAGTGAAAGACTCTTTCACCTTTTAAAAAAGTCTTACCATGATGATCCGATTTTA 183

Qy      1168 AATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCT 1227
Db       184 AATCCTCTAACACCTTGGGAAAGACCACCTCTCAAGAACATATTCTGCATTTATGGCGTA 243

Qy      1228 CATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAAT 1287
Db       244 GATTCGAAGACTGAGGTTGGTTACTATTTTGCACCAAGTGGGAAGCCTTATCCTGATAAT 303

Qy      1288 TGGATCATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACT 1347
Db       304 TGGATTATAACAGATGTGATATATGAAATCGAAGGATCTCTGTATTCCCGGTCAGGAAAT 363

Qy      1348 GTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTC 1407
Db       364 CTGGTTGAAGGAAACCCTGGTGCAACAAGTGGGGATGAGACGGTGCCATACCATTCCCTC 423

Qy      1408 TCTTGGTGCAAGAATTGGCTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAA 1467
Db       424 TCCTGGTGCAAGAATTGGCTGGGGCCAAAAGTGAACATAACAAGGACACCACAGTCAGAG 483

Qy      1468 CACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGT-CAGACAT 1526
Db       484 CATGATGGCTCAGCTGTACAAGTGCATCAAAATATAGAGCATCAACATGGGTGAAGATAT 543

Qy      1527 CATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGA 1586
Db       544 CATTCCCAATATGACAAAGTTAGCTACAATGAAGTACATAACCTATTATGAGGATTCTGA 603

Qy      1587 GAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAA 1629
Db       604 AAGTTTTCCAGGAACGAGAACAGCAGTTTGGGAGCTTGATAAA 646
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RESULT 9
BQ584361
LOCUS BQ584361 565 bp mRNA linear EST 06-DEC-2002
DEFINITION E011859-024-003-K20-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-003-K20 5-PRIME, mRNA sequence.
ACCESSION BQ584361
VERSION BQ584361.1 GI:26113938
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 565)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 565 Std Error: 0.00
Plate: 3 row: K column: 20
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES Location/Qualifiers
source 1. .565
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182335"
/db_xref="taxon:161934"
/clone="024-003-K20"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 21.4%; Score 350.8; DB 5; Length 565;
Best Local Similarity 77.1%; Pred. No. 1.2e-93;
Matches 427; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

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Qy       323 CACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGGTC 382
Db         1 CAAGGCCTGATAGTGGACTCTCTGCAATAACAGAACTTGACCCAGGTTACATAACAGGTC 60

Qy       383 CTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAA 442
Db        61 CTCTCTCCTCTGTGTGGAAAGAATGGGTTAAATGGTGTATTGAGTTTGGTATAGAGCCAA 120

Qy       443 ATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTG 502
Db       121 ATGCAATAATTGCTGTTCCTTATGATTGGAGACTATCACCATCAAAACTTGAGGAACGAG 180

Qy       503 ACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCC 562
Db       181 ACCTTTATTTCCACAAACTCAAGCTGACTTTTGAAACTGCCTACAAACTTCGTGGGGGCC 240

Qy       563 CTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGC 622
Db       241 CGTCATTAGTGTACGCTCATTCACTTGGAAACCTTGTTTTTCGATACTTTCTAGAGTGGT 300

Qy       623 TGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTT 682
Db       301 TGAAGCTTGAAATAGCTCCAAAAGAATATATGAATTGGCTTGATAAACACATCCATGCCT 360

Qy       683 ATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCTCTCTG 742
Db       361 ATTTTGCTGTTGGAGCCCCTTTTCTTGGTGCAACGGAGACGATCAAGGCTGCAATTTTTG 420

Qy       743 GTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTG 802
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Db        421 GTTGCACCTTCGGCGTTCCAGTTTCTGAGGGAACTGCTCGCTTAATGTTCAATTCTTTTG 480

Qy        803 CGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGGGTGATAACACATCCTGGA 862

Db        481 GTTCATCAATGTGGATGTTGCCATTTTCAAAATACTGTAGAACAGATGATAAGTACTGGA 540

Qy        863 CGCATTTTTCTGGG 876

Db        541 AGCACTTTTCTGAG 554


RESULT 10
CD710878
LOCUS       CD710878                560 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  VVA026C02_402285 An expressed sequence tag database for abiotic
            stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
            cDNA clone VVA026C02 5, mRNA sequence.
ACCESSION   CD710878
VERSION     CD710878.1  GI:32245059
KEYWORDS    EST.
SOURCE      Vitis vinifera
  ORGANISM  Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Cramer,G.R. and Cushman,J.C.
  TITLE     An expressed sequence tag database for abiotic stressed leaves of
            Vitis vinifera var. Chardonnay
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
            PCR PRimers
            FORWARD: T3 20mer
            BACKWARD: T7 21mer (backward)
            Plate: 026  row: C  column: 02
            Seq primer: T7 20mer (forward)
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1. .560
                     /organism="Vitis vinifera"
                     /mol_type="mRNA"
                     /db_xref="taxon:29760"
                     /clone="VVA026C02"
                     /tissue_type="leaf"
                     /dev_stage="juvenile and adult"
                     /clone_lib="An expressed sequence tag database for abiotic
                     stressed leaves of Vitis vinifera var. Chardonnay"
                     /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Library construction was performed
                     according to Stratagene's  recommended protocol for the
                     Lambda UniZapXR vector and cDNA synthesis kit."
ORIGIN

  Query Match           20.9%;  Score 343;  DB 6;  Length 560;
  Best Local Similarity   77.2%;  Pred. No. 2.6e-91;
  Matches  429;  Conservative    0;  Mismatches  126;  Indels    1;  Gaps    1;

Qy       1016 CCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATG 1075

Db          5 CTAACATGGAATGTGGACTCCCCACTCAGTTATCCTTCTCCGCTCGTGAGATATCAGATG 64

Qy       1076 GGA-CTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAG 1134

Db         65 GAACCNCTTTTCAAAGCAATAGAGGGTTATGATCCAGATAGCAAGAGGCTCTTGTACCAA 124

Qy       1135 TTAAAGAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCA 1194

Db        125 TTACAGAAGTTATATCATGGTGATCCAGTTTTGAATCCACTTACACCATGGGACAGACCA 184

Qy       1195 CCTATAAAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTAC 1254

Db        185 CCTTTAAAGAACATTTTTTGTATCTATGGAATAAATATAAAGACTGAGGTTGGTTATTAT 244

Qy       1255 TTTGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAA 1314

Db        245 TTTGCACCAAGTGGAAAGCCGTATCCTGATAACTGGATCATGACTGATGTCATTTATGAG 304

Qy       1315 ACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATA 1374

Db        305 ATTGAAGGATCTTTAGTCTCAAGATCAGGAAATCTAGTTGAAGGGAACCCAGGAGCTGCC 364

Qy       1375 ACTGGGGATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCT 1434

Db        365 AGTGGGGATGAGACGGTTCCATACCATTCTCTCTCTTGGTGCAAGAATTGGCTTGGGCCA 424

Qy       1435 AAAGTTAACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAA 1494

Db        425 AAAGTGAACATAACAAGAGCTCCTCAGTCGGAGCATGATGGATCTGACATACAAGTGGAG 484

Qy       1495 CTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGG 1554

Db        485 TTCAATGTAGAACATCATCCTGATGAAGATATAGTTCCCAATATGACAAGGTCACCTCGG 544

Qy       1555 GTTAAGTACATAACCT 1570

Db        545 GTTAAGTATATAACCT 560


RESULT 11
CA090564
LOCUS       CA090564                676 bp    mRNA    linear   EST 23-SEP-2003
DEFINITION  SCSGAM2105C04.g AM2 Saccharum officinarum cDNA clone SCSGAM2105C04
            5', mRNA sequence.
ACCESSION   CA090564
VERSION     CA090564.1  GI:34943871
KEYWORDS    EST.
SOURCE      Saccharum officinarum
  ORGANISM  Saccharum officinarum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
            complex.
REFERENCE   1  (bases 1 to 676)
  AUTHORS   Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
  TITLE     The libraries that made SUCEST
  JOURNAL   Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT     Contact: Arruda P
            Centro de Biologia Molecular e Engenharia Genetica
            Universidade Estadual de Campinas
            Caixa Postal 6010, 13083-970, Campinas SP, Brazil
            Tel: 55 19 3788 1137
            Fax: 55 19 3788 1089
            Email: parruda@unicamp.br
            Clone distribution: clone distribution information can be found
            through the Brazilian Clone Collection Center (BCCC) at
            http://www.bcccenter.fcav.unesp.br
            Plate: 105  row: C  column: 04
            Seq primer: T7 Promoter Primer.
FEATURES             Location/Qualifiers
     source          1. .676
                     /organism="Saccharum officinarum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4547"
                     /clone="SCSGAM2105C04"
                     /lab_host="DH10B"
                     /clone_lib="AM2"
                     /note="Organ: Apical meristem and tissues surrounding of
                     immature plants; Vector: pSport1; Site_1: SalI; Site_2:
                     NotI; An unidirectional cDNA library generated from
```

[Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 20.2%; Score 331.8; DB 6; Length 676;
Best Local Similarity 75.5%; Pred. No. 6.6e-88;
Matches 425; Conservative 0; Mismatches 137; Indels 1; Gaps 1;

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Qy        79 GCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAGCTATCGGGTATAATCATT 138
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Db       114 GCGGCCGGGGCCGACGGCGGCGCGGAGTTCGATTACCGGAAGCTCTCGGGGATCATCATC 173

Qy       139 CCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTTGACTGTCCATACACTCCG 198
             ||||| || ||||| |||||||| || |||||||| |||| || || || ||| | ||
Db       174 CCGGGGTTCGCGTCCACGCAGCTGCGCGCGTGGTCGGTCCTCGATTGCCCCTACTCGCCC 233

Qy       199 TTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACTAAGCTTCTTTCTGCTGTC 258
             || |||||||| || || ||| ||| ||||| |||||| | |||||| | || || ||
Db       234 TTCGACTTCAACCCCCTAGACTCCGTCTGGCTTGACACCGCCAAGCTTTTCTCCGCGGTA 293

Qy       259 AACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAAACAGACCATCCCGAGTGT 318
             || |||||| |||| || ||| |||| || || |||||||| |||||||||| || ||
Db       294 AATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAATCAGACAGACCATCCGGAATGC 353

Qy       319 AAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACA 378
             |||||| ||||||| |||||||||| || || ||||| ||||| || ||||| ||||||
Db       354 AAGTCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAGTTGGACCCTGGTTATATAACA 413

Qy       379 GGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAA 438
             |||||||  ||| | || |||||||| ||| | || |||||||| |||||||| || |||
Db       414 GGTCCTCGCTCTTCAGTATGGAAAGAATGGGTCAAATGGTGTGTAGAGTTTGGCATTGAA 473

Qy       439 GCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAG 498
             || ||||||||| ||||||| || || |||||||| || | ||| | |   | || |||
Db       474 GCTAATGCAATTATCGCTGTCCCGTATGATTGGAGACTGCCCCCATCAATCCTTGAGGAG 533

Qy       499 CGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACT-CCGTGG 557
             || || || |  |||||||  | ||||| || ||||||  || ||| ||||| ||| ||
Db       534 CGAGATCTGTTTTTTCACAAATTAAAGTTTACTTTTGAACTTGTTTTGAAACTCCCGCGG 593

Qy       558 CGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGA 617
               || || ||| | |||||||| | ||| |||| |||||||| ||  | |||||| ||||
Db       594 AGGGCCATCTTTGGTATTTGCTCTTTCGATGGCAAATAATGTGTTTCGCTACTTTTTGGA 653

Qy       618 ATGGCTGAGGCTAGAAATTGCAC 640
             |||  |||  || |||| ||| |
Db       654 ATGCTTGAAACTGGAAAATGCCC 676
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RESULT 12
AI974291
LOCUS AI974291 534 bp mRNA linear EST 26-AUG-1999
DEFINITION T110293e KV0 Medicago truncatula cDNA clone pKV0-1E14, mRNA sequence.
ACCESSION AI974291
VERSION AI974291.1 GI:5776732
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 534)
AUTHORS VandenBosch,K., Hur,J., Moore,J., Beremand,P., Peng,H. and Ellis,L.
TITLE ESTs from uninoculated roots of Medicago truncatula (1999b)
JOURNAL Unpublished (1999)

COMMENT Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
Other name: 07-B-7; date: 6/30/99; Submitted to the Database of Expressed Sequence Tags (dbEST) on 08/25/99; More information is available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).

FEATURES Location/Qualifiers
source 1. .534
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV0-1E14"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XLOLR"
/clone_lib="KV0"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

ORIGIN

Query Match 19.3%; Score 316.4; DB 1; Length 534;
Best Local Similarity 76.3%; Pred. No. 2.6e-83;
Matches 389; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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Qy       989 TTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTGT 1048
             || ||||||    |     | |||| || || | ||||||||||| || || || |  || |
Db        25 TTTCAGAAATCCCCGAGGCCAACTTGTCCGGAATGGAATGTGGACTACCTACTCAATTAT 84

Qy      1049 CTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACC 1108
             ||||| |||| |||||| |||| |||||   |  ||||||| ||||| ||||| |||||||
Db        85 CTTTCTCAGCTCGTGAAATAGCGGATGGCTCCTTTTTCAAGGCAATTGAAGATTATGACC 144

Qy      1109 CAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTTA 1168
             |||| ||||||||  | ||  |||| ||| |||| |  |||| || ||| |||||  |||
Db       145 CAGACAGCAAGAGACTCTTGTACCAATTAGAGAAATCATATCTTGGTGATCCTGTACTTA 204

Qy      1169 ATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCTC 1228
             |||| || || |||||||  | ||||| |||||||| || || ||||| |||||   |
Db       205 ATCCACTTACACCTTGGGATCGGCCACCAATAAAAAACGTGTTCTGCATTTATGGCAGTA 264

Qy      1229 ATCTAAAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAATT 1288
             ||  ||||||| |||||||||| |||||||||| || ||||| || |||||||||| |
Db       265 ATTCAAAGACAAAGGTTGGTTACTACTTTGCCCCTAGCGGCAAGCCGTATCCTGATAACT 324

Qy      1289 GGATCATCACGGATATCATTTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACTG 1348
             ||||||| || ||| || |||| ||    ||||| || || ||  |||||| |||| |
Db       325 GGATCATTACAGATGTCGTTTATGAGTACGAAGGATCTCTAGTCACAAGGTCAGGAAATC 384

Qy      1349 TGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTCT 1408
             ||||||| ||||| |||| |||||| ||| |||||||||| || ||  | || || |
Db       385 TGGTTGAAGGGAACCCTGGATCTATAAGTGGCGATGAGACGGTTCCATACAACTCCCTAT 444

Qy      1409 CTTGGTGCAAGAATTGGCTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGAAC 1468
             ||||||||| |||||||| ||||| || || ||||| |||| |||||| ||| ||||||
Db       445 CTTGGTGCAAAAATTGGCTGGGACCAAAGGTGAACATTACAAGAGCTCCTCAGTCAGAAC 504

Qy      1469 ACGATGGAAGCGACGTACATGTGGAACTAA 1498
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Db       505 ACGATGGCTCAGATGTACAGATTGATTTGA 534
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RESULT 13
BI267124
LOCUS       BI267124                628 bp    mRNA    linear   EST 18-JUL-2001
DEFINITION  NF097C07IN1F1054 Insect herbivory Medicago truncatula cDNA clone
            NF097C07IN 5', mRNA sequence.
ACCESSION   BI267124
VERSION     BI267124.1  GI:14871872
KEYWORDS    EST.
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 628)
  AUTHORS   Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
            Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
  TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula insect herbivory library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Korth K
            Dept. of Plant Pathology
            University of Arkansas
            217 Plant Science Building, Fayetteville, AR 72701, USA
            Tel: 501 575 5191
            Fax: 501 575 7601
            Email: kkorth@comp.uark.edu
            Insert Length: 628   Std Error: 0.00
            Plate: 097  row: C  column: 07
            Seq primer: TCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .628
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /db_xref="taxon:3880"
                     /clone="NF097C07IN"
                     /tissue_type="local and systemic leaves"
                     /dev_stage="mature"
                     /clone_lib="Insect herbivory"
                     /note="Vector: Lambda Zap; Library was produced from fully
                     expanded M. truncatula leaves of plants fed upon by
                     Spodoptera exigua (beet armyworm) for 24 hours. Systemic
                     (undamaged leaves from injured plants) and wounded leaves
                     were harvested and pooled."
ORIGIN

  Query Match             18.7%;  Score 306.6;  DB 4;  Length 628;
  Best Local Similarity   79.2%;  Pred. No. 2.5e-80;
  Matches  374;  Conservative    0;  Mismatches   97;  Indels    1;  Gaps    1;

Qy        108 CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGC 167
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Db        149 CGATTACTCTAAACTCTCCGGCATTATTATCCCAGGCTTCGCTTCTACTCAGCTTCGAGC 208

Qy        168 GTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATG 227
              ||||| || |||||||| || ||| ||||| | || |||||||| |||||  | || ||
Db        209 ATGGTCTATTCTTGACTGCCCTTACTCTCCGCTAGATTTCAATCCTCTCGATTTGGTTTG 268

Qy        228 GCTAGACACCACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGA 287
              ||| |||||||| || |||||||||||||| || || ||| ||||||| ||| || | ||
Db        269 GCTCGACACCACCAAACTTCTTTCTGCTGTGAATTGTTGGCTTAAGTGCATGTTGTTGGA 328

Qy        288 TCCTTATAATCAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGC 347
              ||||| |||||||||| ||||| || ||||| || || ||||| || |||||||| |
Db        329 CCCTTACAATCAAACAGATCATCCTGATTGTAAATCCCGTCCTGATAGCGGTCTTTCCGG 388

Qy        348 CATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTG 407
              || |||||  | |||||||||| |||||||| ||||||||  |||| |||||||| ||
Db        389 AATTACAGAGCTTGATCCAGGTTATATAACAGGACCTCTTTCGTCTGTATGGAAAGAATG 448

Qy        408 GCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGA 467
              | |||||||||||| |||| ||||| ||| |||| ||||||||  | |||||||| || ||
Db        449 GATTAAGTGGTGTATTGAATTTGGCATANAAGCTAATGCAATAATTGCTGTTCCTTATGA 508

Qy        468 TTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTT 527
              ||||||| |||||||| |||   | ||||| || |||||||||||||| ||||| || ||
Db        509 TTGGAGACTGTCACCATCCATGCTTGAAGAACGAGACCTTTACTTTCATAAGCTTAAATT 568

Qy        528 GACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCC 579
              ||| ||||| |||||||| |||| || || ||||| ||| || | |||| |
Db        569 GACATTTGAGACTGCTTT-CAACTTCGAGGNGGCCCCTCTTTANTTTTTGGC 619


RESULT 14
AU306500
LOCUS       AU306500                728 bp    mRNA    linear   EST 22-JAN-2004
DEFINITION  AU306500 zinnia cultured mesophyll cell equalized cDNA Zinnia
            elegans cDNA clone Z16086, mRNA sequence.
ACCESSION   AU306500
VERSION     AU306500.1  GI:41122436
KEYWORDS    EST.
SOURCE      Zinnia elegans
  ORGANISM  Zinnia elegans
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Zinnia.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Demura,T., Tashiro,G., Horiguchi,G., Kishimoto,N., Kubo,M.,
            Matsuoka,N., Minami,A., Nagata-Hiwatashi,M., Nakamura,K.,
            Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
            Fukuda,H.
  TITLE     Visualization by comprehensive microarray analysis of gene
            expression programs during transdifferentiation of mesophyll cells
            into xylem cells
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
COMMENT     Contact: Taku Demura
            Morphogenesis Research Group
            RIKEN Plant Science Center
            1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9605
            Fax: 81-45-503-9573
            Email: demura@postman.riken.go.jp
            This clone was obtained at our laboratory
            Seq primer: M13 forward.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Zinnia elegans"
                     /mol_type="mRNA"
                     /cultivar="Canary bird"
                     /db_xref="taxon:34245"
                     /clone="Z16086"
                     /tissue_type="mesophyll cell"
                     /clone_lib="zinnia cultured mesophyll cell equalized cDNA"
                     /note="Vector: pGEM-T easy; cultured in tracheary element
                     differentiation-inductive medium"
ORIGIN

  Query Match             17.9%;  Score 293.4;  DB 1;  Length 728;
  Best Local Similarity   70.3%;  Pred. No. 2.5e-76;
  Matches  484;  Conservative    0;  Mismatches  182;  Indels   22;  Gaps    6;

Qy        442 AATGCAATTGTCGCTGT-TCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCG 500
              ||||| ||| | ||||| ||||| ||||||||| |||||||| | ||| | || |||||
Db          1 AATGCTATTCTTGCTGTGNCCATATGATTGGAGACTGTCACCATCGAAACTTGAGGAGCG 60

Qy        501 TGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGG 560
              ||  | ||||| |||||||||||  | || |||||||| ||| | ||||  ||||| ||
Db         61 GGATTTGTACTTCCACAAGCTCAAACTTACATTTGAAACAGCTCTTAAACATCGTGGTGG 120

Qy        561 CCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTT-TCTGGAAT 619
              || || || |||||||||||| ||  ||||||| ||||| ||  | ||||| | | || |
Db        121 TCCATCCATCGTATTTGCCCACTCTCTGGGTAACAATGTTTTTCGGTACTTNTTTAGAGT 180

Qy        620 GGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATG 679
              || ||| |||||||||| | ||||||   ||| |  | ||||| ||| | ||||| || |
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Db        181 GGTTGAAGCTAGAAATTTCTCCAAAAAGATATATCCAATGGCTAGATGATCATATACACG 240

Qy        680 CTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCTCT 739

Db        241 CTTACTTTGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTCAGACAGTAGAAGCAACACTCT 300

Qy        740 CTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTCTT 799

Db        301 CTGGTTCCACTTTTGGTCTTCCTATACCCGAGGGGACGGCCCGGTTGATGTTCAATTCAT 360

Qy        800 TTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGGGTGATAACACATCCT 859

Db        361 TCGGCTCTTCACTATGGATGTCACCTTTTTCAAAGTATTGTACGAGTGAAAACGTCTACT 420

Qy        860 GGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATGAAG 919

Db        421 CAAAGCATTTTTCTGGTGGGCGCAGAAAAAAACACAA---TGTATATCAGTGTGATGATC 477

Qy        920 AGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTC--- 976

Db        478 TTGAATATCGGTTAAACTATTCTGGATTTCCAACTAACATAATCAATATTGAGATCCCGT 537

Qy        977 ------------CTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGG 1024

Db        538 CAGTATTAGAAGCTTATCCATCCTTTGGAGATGAAATGCAGGCCAATTTATCTAACATGG 597

Qy       1025 AATGTGGCCTTCCCAC-CCTTTTGTCTTTCACAGCCCGTGAACTAGCAGAT-GGGACTCT 1082

Db        598 AATGTGGGGTCCCCACTCAATTTATCCTTTTCTGCTCGTGAAATAGCAGATGGGGACTTT 657

Qy       1083 TTTCAAAGCAATAGAAGACTATGACCCA 1110

Db        658 TTTTAAAGCGATTGAGGATTATGATCTA 685
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RESULT 15
CA221313
LOCUS CA221313 683 bp mRNA linear EST 25-SEP-2003
DEFINITION SCSGFL4034D01.g FL4 Saccharum officinarum cDNA clone SCSGFL4034D01 5', mRNA sequence.
ACCESSION CA221313
VERSION CA221313.1 GI:35275497
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 683)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 034 row: D column: 01
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .683
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCSGFL4034D01"
/lab_host="DH10B"
/clone_lib="FL4"
/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN

Query Match 17.8%; Score 291.8; DB 6; Length 683;
Best Local Similarity 66.6%; Pred. No. 7.3e-76;
Matches 457; Conservative 0; Mismatches 205; Indels 24; Gaps 2;

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Qy        552 CCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTT 611

Db          1 CCGAGGAGGGCCATCTTTGGTATTTGCTCATTCGATGGGAAATAATGTGTTTCGCTACTT 60

Qy        612 TCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCA 671

Db         61 TTTGGAATGGTTGAAACTGGAAATTGCTCCCAAGCACTATATCCAGTGGCTTGATGAACA 120

Qy        672 TATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATC 731

Db        121 TATACATGCATACTTTGCAGTTGGCGCTCCTCTTCTTGGATCTACTGAAGCAGTTAGAGG 180

Qy        732 TACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTTGTTGTC 791

Db        181 TGCTCTTTCTGGAACAACTTTTGGTCTTCCAGTCAGTGAGGGCACAGCACGATTGATGTT 240

Qy        792 CAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGGGTGATAA 851

Db        241 TAATGCATTTGGTTCTTCTCTATGGCTTATGCCATTCTCAAAACACTGCAAAGCTGATAA 300

Qy        852 CACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTG 911

Db        301 TATCTACTGGAAGCATTTTTTTGAGGGAAAGGGA---GGTTGTCCTCACAGACAACAATG 357

Qy        912 TGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGA 971

Db        358 TGATGAAGCTGAATATATNTCAGACTACGCCGGATGGCCCACAGACCTTGTTAATATTGA 417

Qy        972 AATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGA---------------- 1015

Db        418 GGTTCCTTCAGTTCGAGATATGGGGGCATACCCATCCATCACGGATATAACCGAGAACAT 477

Qy       1016 -----CCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGC 1070

Db        478 AACATCCAGTATGGAGTGCGGAAAGCCAACTCTCCTGTCATNTTCTGCCAGAGAAGTGTC 537

Qy       1071 AGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACA 1130

Db        538 AGATGGTACTTTGTTCAGAACAATAGAGGATTATGACCCTCAGAGCAAGGCACTTGGTTA 597

Qy       1131 CCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAG 1190

Db        598 TCAGCTTGAGAAGTATTATCAGGGTGATCCAGTTCTGAACCCTCTAAACACCTGNGAGAG 657

Qy       1191 ACCACCTATAAAAAATGTATTTTGCA 1216

Db        658 AACCCCAATAAAGAACATATTTGGCA 683
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:40:26 ; Search time 7037 Seconds
(without alignments)
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Title: US-09-651-651-4
Perfect score: 1641
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	271.8	16.6	3896	6	BD271623	BD271623 Novel cla
	4	271.8	16.6	3896	6	BD271633	BD271633 Novel cla
	5	271.8	16.6	3896	6	AX037587	AX037587 Sequence
	6	271.8	16.6	3896	6	AX037606	AX037606 Sequence
	7	271.8	16.6	119914	8	AC003027	AC003027 Arabidops
	8	176.2	10.7	328	6	AX090328	AX090328 Sequence
c	9	118	7.2	93398	8	AP006356	AP006356 Lotus cor
c	10	113.4	6.9	118192	8	AP004120	AP004120 Oryza sat
c	11	113.4	6.9	147123	8	AP005691	AP005691 Oryza sat
c	12	113.4	6.9	158971	2	AP004882	AP004882 Oryza sat
	13	110.4	6.7	709	6	BD271624	BD271624 Novel cla
	14	110.4	6.7	709	6	BD271634	BD271634 Novel cla
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	16	110.4	6.7	709	6	AX037607	AX037607 Sequence
	17	109	6.6	356	6	AX090329	AX090329 Sequence
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c	19	68	4.1	110000	8	CR382131_19	Continuation (20 o
	20	59	3.6	110000	8	CR382136_07	Continuation (8 of
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c	22	57.8	3.5	110000	8	CR382126_06	Continuation (7 of
c	23	52.6	3.2	733	8	AF428124	AF428124 Swietenia
	24	49.4	3.0	1986	6	BD271616	BD271616 Novel cla
	25	49.4	3.0	1986	6	BD271625	BD271625 Novel cla
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	28	49.4	3.0	1986	6	AX037595	AX037595 Sequence
	29	49.4	3.0	1986	6	AX037597	AX037597 Sequence
	30	49.4	3.0	1986	6	AX090382	AX090382 Sequence
c	31	49.4	3.0	2000	6	AX655393	AX655393 Sequence
	32	49.4	3.0	2575	8	SCYNR008W	Z71623 S.cerevisia
	33	49.4	3.0	23901	8	SCN201952	X77395 S.cerevisia
	34	47.4	2.9	2000	6	AX655393	AX655393 Sequence
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	40	47.2	2.9	5907	10	RATCPE01	L07273 Rattus norv
c	41	47.2	2.9	261278	2	AC107586	AC107586 Rattus no
c	42	43.4	2.6	110000	8	CR380955_05	Continuation (6 of
c	43	43.4	2.6	300029	8	AE016899	AE016899 Eremothec
c	44	42.8	2.6	1737	8	AY259955	AY259955 Argyroxip
c	45	42.8	2.6	1737	8	AY259956	AY259956 Argyroxip

ALIGNMENTS

RESULT 1
AX090311
LOCUS AX090311 1641 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 4 from Patent WO0116308.
ACCESSION AX090311
VERSION AX090311.1 GI:13444180
KEYWORDS .
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Lassner,M. and van Eenennaam,A.
TITLE Plant sterol acyltransferases
JOURNAL Patent: WO 0116308-A 4 08-MAR-2001;
MONSANTO COMPANY (US)
FEATURES Location/Qualifiers
source 1. .1641
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN

Query Match 100.0%; Score 1641; DB 6; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
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Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
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Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
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Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
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Qy        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600
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Qy        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720
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Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
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RESULT 2
AF493159

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LOCUS       AF493159               2609 bp    mRNA    linear   PLN 02-DEC-2002
DEFINITION  Medicago truncatula putative phosphatidylcholine acyltransferase
            mRNA, complete cds.
ACCESSION   AF493159
VERSION     AF493159.1  GI:25992000
KEYWORDS    .
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 2609)
  AUTHORS   Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriel,A.
  TITLE     Acyltransferases involved in lipid (sterol) biosynthesis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2609)
  AUTHORS   Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriel,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2002) Plant Molecular Biology Institute, CNRS, 28
            rue Goethe, Strasbourg 67083, France
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ORIGIN

Query Match 55.6%; Score 911.8; DB 8; Length 2609;
Best Local Similarity 75.6%; Pred. No. 1.8e-253;
Matches 1167; Conservative 0; Mismatches 352; Indels 24; Gaps 2;

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Qy       768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
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Qy       828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
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Qy       888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
Db       948 ---AGGTACCAATACATATCACTGTGATGAGGAGGAGTTTAAGTCAAACTTTTCTGGATG 1004

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Qy       989 --TTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTT 1046
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Qy      1047 GTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGA 1106
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Qy      1107 CCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGTTGTATCATGATGACCCTGTTTT 1166
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Qy      1407 CTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTTAACATAACAATGGCTCCCCAGCCAGA 1466
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Qy      1467 ACACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACAT 1526
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Qy      1527 CATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGA 1586
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RESULT 3
BD271623
LOCUS BD271623 3896 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271623
VERSION BD271623.1 GI:33081391
KEYWORDS JP 2002541783-A/8.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 3896)
AUTHORS Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
TITLE Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme
JOURNAL Patent: JP 2002541783-A 8 10-DEC-2002;
BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/8
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR 07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI -,HANS RONNE,STEN STYMNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
Novel class enzyme in biosynthesis pathway

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           of triacrylglycerol
           CC           production
           CC   and recombinant DNA molecule encoding the enzyme FH   Key
                  Location/Qualifiers
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           FT                   /organism='Arabidopsis thaliana (thale  FT
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             16.6%;  Score 271.8;  DB 6;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 2.7e-67;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
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Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
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RESULT 4
BD271633
LOCUS       BD271633               3896 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel class enzyme in biosynthesis pathway of triacrylglycerol
            production and recombinant DNA molecule encoding the enzyme.
ACCESSION   BD271633
VERSION     BD271633.1  GI:33081401
KEYWORDS    JP 2002541783-A/18.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 3896)
  AUTHORS   Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
  TITLE     Novel class enzyme in biosynthesis pathway of triacrylglycerol
            production and recombinant DNA molecule encoding the enzyme
  JOURNAL   Patent: JP 2002541783-A 18 10-DEC-2002;
            BASF PLANT SCIENCE GMBH
COMMENT     OS   Arabidopsis thaliana (thale cress)
            PN   JP 2002541783-A/18
            PD   10-DEC-2002
            PF   28-MAR-2000 JP 2000609586
            PR   01-APR-1999 EP   99106656.4,10-JUN-1999 EP   99111321.8 PR
            07-FEB-2000 US    60/180687
            PI   ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI
            ,HANS RONNE,STEN STYMNE
            PC   C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC
            (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
            Novel class enzyme in biosynthesis pathway
            of triacrylglycerol
            CC           production
            CC   and recombinant DNA molecule encoding the enzyme FH   Key
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ORIGIN

  Query Match             16.6%;  Score 271.8;  DB 6;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 2.7e-67;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
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Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
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Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
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Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------------------- 987
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Db       1967 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 2026

Qy        988 ------------------------------------------------------------ 987

Db       2027 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 2086

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RESULT 5
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LOCUS       AX037587               3896 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 11 from Patent WO0060095.
ACCESSION   AX037587
VERSION     AX037587.1  GI:11227006
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Banas,A., Stahl,U., Stymne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
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  TITLE     A new class of enzymes in the biosynthetic pathway for the
            production of triacylglycerol and recombinant dna molecules
            encoding these enzymes
  JOURNAL   Patent: WO 0060095-A 11 12-OCT-2000;
            BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
            STYMNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
            ANDERS (SE)
FEATURES             Location/Qualifiers
     source          1. .3896
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ORIGIN

  Query Match             16.6%;  Score 271.8;  DB 6;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 2.7e-67;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
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Db       1787 TCAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 1846

Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
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Db       1847 TTCAAAGAATTGCAAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAA 1906

Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
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Db       1907 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 1966

Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------------------- 987
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Db       1967 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 2026

Qy        988 ------------------------------------------------------------ 987

Db       2027 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 2086

Qy        988 ------------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
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Db       2087 GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 2146

Qy       1036 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
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Db       2147 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 2206

Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
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Db       2207 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 2255


RESULT 6
AX037606
LOCUS       AX037606               3896 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 30 from Patent WO0060095.
ACCESSION   AX037606
VERSION     AX037606.1  GI:11227020
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Banas,A., Stahl,U., Stymne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
  TITLE     A new class of enzymes in the biosynthetic pathway for the
            production of triacylglycerol and recombinant dna molecules
            encoding these enzymes
  JOURNAL   Patent: WO 0060095-A 30 12-OCT-2000;
            BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
            STYMNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
            ANDERS (SE)
FEATURES             Location/Qualifiers
     source          1. .3896
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"
ORIGIN

  Query Match             16.6%;  Score 271.8;  DB 6;  Length 3896;
  Best Local Similarity   80.0%;  Pred. No. 2.7e-67;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
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Db       1787 TCAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 1846

Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
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Db       1847 TTCAAAGAATTGCAAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAA 1906

Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1907 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 1966

Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------------------- 987
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Db       1967 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 2026

Qy        988 ------------------------------------------------------------ 987

Db       2027 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 2086

Qy        988 ------------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
                          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2087 GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 2146

Qy       1036 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
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Db       2147 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 2206

Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
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Db       2207 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 2255


RESULT 7
AC003027
LOCUS       AC003027               119914 bp    DNA     linear   PLN 30-OCT-2002
DEFINITION  Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence,
            complete sequence.
ACCESSION   AC003027
VERSION     AC003027.1  GI:4079614
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,
            Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
            Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V.,
            Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA
            Sequencing and Technology Center, 855 California Avenue, Palo Alto,
            CA 94304, USA
REFERENCE   3  (bases 1 to 119914)
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  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1998) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
REFERENCE   4  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     On Dec 30, 1998 this sequence version replaced gi:2734094.
            Bases 1-9262 of clone F21M11 overlap with bases 68998-78259 of
            'TAMU' BAC clone F20D22 (AC002411) and bases 119525-119914 of clone
            F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
            (AC002560).
            e-mail for correspondence: arab@sequence.stanford.edu
            Genes with similarity to proteins in the databases are described as
            'putative', '-like' or 'similar to'.  Genes that have EST
            similarity but no significant protein similarity are described as
            'unknown proteins'.  Genes that are annotated based only on gene
            prediction software are described as 'hypothetical proteins'.
            The software programs used to predict genes include:  Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
            http://gnomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev
            & A.Salamov, Sanger Centre,  http://genomic.sanger.ac.uk/), and
            NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
FEATURES              Location/Qualifiers
     source           1. .119914
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                      /mol_type="genomic DNA"
                      /cultivar="Columbia"
                      /db_xref="taxon:3702"
                      /chromosome="I"
                      /clone="F21M11"
     misc_feature     1. .9262
                      /note="overlap with bases 68998-78259 of 'IGF' BAC clone
                      F21M11."
     misc_feature     1. .7000
                      /note="Proteins in this region are annotated in the F21M11
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     gene             7684. .10913
                      /gene="F21M11.1"
     CDS              join(7684. .7866,7965. .8027,8122. .8160,8250. .8381,
                      8458. .8728,8875. .9893,10003. .10256,10344. .10410,
                      10501. .10551,10685. .10781,10885. .10913)
                      /gene="F21M11.1"
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                      VRRNGERGLAMTVYNNASPSSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
                      EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
                      SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
                      VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
                      ECEISGDGWKAISNMKDITAGEENVEIPWVNEINEKVPSRFRYMPHSFVFQDAPVIFS
                      LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDQ
                      RKQVLRFCEECPLERAKKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRGMHN
                      KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
                      WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
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                      /gene="F21M11.2"
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                      16327. .16362))
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                      LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
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     gene             complement(16835. .20238)
                      /gene="F21M11.4"
     CDS              complement(join(16835. .17185,17274. .17392,17491. .17656,
                      17795. .17885,17982. .18079,18175. .18361,18504. .18604,
                      18705. .19049,19134. .19349,19439. .19791,19862. .19967,
                      20188. .20238))
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                      /note="Hypothetical protein"
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                      FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNPKTQDP
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                      SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKW
                      IINAAWMKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRAETNKPKLFEGLKFYFF
                      GDFYKGYKEDLQNLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVYNIDPPHGCAL
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     CDS              join(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
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     CDS             28007. .28465
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  Query Match           16.6%;  Score 271.8;  DB 8;  Length 119914;
  Best Local Similarity   80.0%;  Pred. No. 3e-67;
  Matches  375;  Conservative    0;  Mismatches    2;  Indels   92;  Gaps    1;

Qy        768 TGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 827
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22538 TCAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATT 22597

Qy        828 TTCAAAGAATTGCAAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAA 887
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db      22598 TTCAAAGAATTGCAAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAA 22657

Qy        888 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 947
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Db      22658 GAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTG 22717

Qy        948 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGC---------------------- 987
              |||||||||||||||||||||||||||||||||||||||
Db      22718 GCCGACAAATATTATTAACATTGAAATTCCTTCCACTAGCGGTTAGACTCTGTATATGCA 22777

Qy        988 ------------------------------------------------------------ 987

Db      22778 ACTGTAACACTAACAAAAGTTTCACCAAGAATGTTCACTCTCATATTTCGTTCCTTTGAT 22837

Qy        988 ------------GTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 1035
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Db      22838 GTGTATCCATCAGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTT 22897

Qy       1036 CCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATA 1095
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1096 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144
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Db      22958 GAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 23006


RESULT 8
AX090328
LOCUS       AX090328                328 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 21'from Patent WO0116308.
ACCESSION   AX090328
VERSION     AX090328.1  GI:13444194
KEYWORDS    .
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1
  AUTHORS   Lassner,M. and van Eenennaam,A.
  TITLE     Plant sterol acyltransferases
  JOURNAL   Patent: WO 0116308-A 21 08-MAR-2001;
            MONSANTO COMPANY (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           10.7%;  Score 176.2;  DB 6;  Length 328;
  Best Local Similarity   79.0%;  Pred. No. 1.6e-39;
  Matches  222;  Conservative    0;  Mismatches   58;  Indels    1;  Gaps    1;

Qy        238 ACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAAT 297
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Db         35 ACATTGCTTTTCTCTGCGGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAAT 94

Qy        298 CAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAA 357
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Db         95 CAGATAGACCATCCCGAATGCAAGTCAAGGCCTGATAGTGGTC-TTCTGCAATTACAGAG 153

Qy        358 TTGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGG 417
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Qy        418 TGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTG 477
              ||||| |||||||| || ||||| ||||||||| |||||||||| || ||||||||| ||
Db        214 TGTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCGTATGATTGGAGACTG 273

Qy        478 TCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAA 518
              | ||| | |   | || ||| | || || ||||||||||
Db        274 CCCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAA 314


RESULT 9
AP006356/c
LOCUS       AP006356                93398 bp    DNA     linear   PLN 22-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus genomic DNA, chromosome 6,
            clone:LjT06I08, TM0082b, complete sequence.
ACCESSION   AP006356
VERSION     AP006356.1  GI:31580987
KEYWORDS    HTG.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Asamizu,E., Kato,T., Sato,S., Nakamura,Y., Kaneko,T. and Tabata,S.
  TITLE     Structural Analysis of a Lotus japonicus Genome. IV. Sequence
            Features and Mapping of seventy-three TAC clones which cover the
            7.5 Mb Regions of the Genome
  JOURNAL   DNA Res. (2003) In press
REFERENCE   2  (bases 1 to 93398)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute,
            Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
            Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
            Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .93398
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="genomic DNA"
                     /variety="japonicus"
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                     /db_xref="taxon:34305"
                     /chromosome="6"
                     /clone="LjT06I08"
                     /clone_lib="LjT library"
                     /note="TM0082b, a part of TAC clone:TM0082.~synonym: Lotus
                     japonicus"
ORIGIN

  Query Match             7.2%;  Score 118;  DB 8;  Length 93398;
  Best Local Similarity   79.9%;  Pred. No. 1.6e-22;
  Matches  139;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy        522 CAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCA 581
              ||  ||||| |||||||||||||  ||||| || || ||||| ||| |||| ||||||||
Db      32553 CAGATTGACATTTGAAACTGCTTATAAACTTCGAGGTGGCCCCTCTTTAGTTTTGCCCA 32494

Qy        582 TTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACC 641
              |||| |||||||| | || ||  | || ||  |||| ||| ||| |||||| || |||||
Db      32493 TTCATTGGGTAATCACGTTTTTCGTTATTTCTTGGAGTGGTTGAAGCTAGAGATAGCACC 32434

Qy        642 AAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG 695
              ||||||||||||  | ||||| ||||| |||| || || ||||| ||||||||
Db      32433 AAAACATTATTTCGAATGGCTGGATCAACATATTCACGCATATTTTGCTGTTGG 32380


RESULT 10
AP004120/c
LOCUS       AP004120              118192 bp    DNA     linear   PLN 02-JUN-2004
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
            BAC clone:OJ1293_E04.
ACCESSION   AP004120
VERSION     AP004120.3  GI:47847857
KEYWORDS    .
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
            clone:OJ1293_E04
  JOURNAL   Published Only in Database (2001)
REFERENCE   2  (bases 1 to 118192)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2001) Takuji Sasaki, National Institute of
            Agrobiological Sciences, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     On Jun 1, 2004 this sequence version replaced gi:34740243.
            Genes were predicted from the integrated results of the following:
            GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
            (http://www.softberry.com/), GeneMark.hmm
            (http://opal.biology.gatech.edu/GeneMark/), GlimmerM
            (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM
            (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
            (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
            (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
            (http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The
            genomic sequence was searched against NCBI NonRedundant Protein
            database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
            sequence database at RGP or DDBJ. Protein homologies of the coding
            regions were searched against NCBI NonRedundant Protein database
            with BLASTP. ESTs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
            Full-length cDNAs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no.
            A gene with identity or significant homology to a protein is
            classified based on the protein name to indicate the homology level
            such as same name, 'putative-' and '-like protein'.  A gene without
            significant homology to any protein but with full-length cDNA or
            EST homology (covering almost the entire length of partial
            sequence) is classified as an 'unknown' protein. A gene predicted
            by two or more gene prediction programs is classified as a
            'hypothetical' protein according to IRGSP standard. A gene
            predicted by a single gene prediction program is also classified as
            a probable 'hypothetical' protein and is included as a
            miscellaneous feature of the sequence.
            The orientation of the sequence is from -21M13 to M13rev of the BAC
            clone. This sequence of OJ1293_E04 clone has an overlap with
            OSJNBa0053L11 (DDBJ: AP005691) clone at 5' end and with P0643F09
            (DDBJ: AP005111) at 3' end. The sequence was generated by combining
            Monsanto and RGP-Japan sequencing data. Detailed information on
            overlap and assembly quality together with annotation of this entry
            is available at
            http://rgp.dna.affrc.go.jp/GenomeSeq.html.
FEATURES             Location/Qualifiers
     source          1. .118192
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="genomic DNA"
                     /cultivar="Nipponbare"
                     /db_xref="taxon:39947"
                     /chromosome="2"
                     /clone="OJ1293_E04"
     gene            1863. .2468
                     /gene="OJ1293_E04.1"
     mRNA            join(<1863. .1936,2024. .>2468)
                     /gene="OJ1293_E04.1"
                     /note="start and end point are not identified"
     CDS             join(1863. .1936,2024. .2468)
                     /gene="OJ1293_E04.1"
                     /note="predicted by GeneMark.hmm etc."
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="BAD21651.1"
                     /db_xref="GI:47847858"
                     /translation="MELRQNCVQKLGDSKVPWKFVPDFPFSEVVEFLKGYRVEVCGKI
                     PCKMLSGNSNYAAYIVFVVAEDSCGLASVWVATVGVGGRQSTRQVCLDSSNRNDYYYE
                     GEIEVPQDGSVILPQERADGWMELELGEFYNQEGNNQGEVCFSLVKPKAGRWLSNGGL
                     VIQGIEIRPKIS"
     gene            join(6482. .6988,7071. .7653,7919. .8032,8112. .8419,
                     8501. .8573,8672. .9312)
                     /gene="OJ1293_E04.2"
     misc_feature    join(6482. .6988,7071. .7653,7919. .8032,8112. .8419,
                     8501. .8573,8672. .9312)
                     /gene="OJ1293_E04.2"
                     /note="transposase-like"
     gene            11875. .13972
                     /gene="OJ1293_E04.3"
     mRNA            join(11875. .12242,12368. .12486,13292. .13972)
                     /gene="OJ1293_E04.3"
                     /note="supported by full-length cDNA(s): AK060823"
     mRNA            join(11953. .12242,12368. .12486,13292. .13962)
                     /gene="OJ1293_E04.3"
                     /note="supported by full-length cDNA(s): AK098981"
     CDS             join(11964. .12242,12368. .12486,13292. .13787)
                     /gene="OJ1293_E04.3"
                     /note="contains EST(s): AU092429(C50563)
                     contains full-length cDNA(s): AK060823,AK098981
                     phloem-specific lectin"
                     /codon_start=1
                     /product="F-box family protein-like"
                     /protein_id="BAD21652.1"
                     /db_xref="GI:47847859"
                     /translation="MEEEGEGLCEIARLPEELLSAAISRASPRDACHAAAVSPAFRAA
                     ADSDAVWASFLPRNLPDLADGELSPAPASKKELFLRLSDGPYLLSDRLMSMWLDRETG
                     AKCYMLSARSLVIIWGDTPHYWRWIPLTDSRFAEGAELIDVCWLEIRGRIHSKMLSPN
                     STYAAYMVFKIADEFYGLDAPFQEASVSLGGRGSTKIVCVQSYDSEDEEVPENYWPMS
                     IGPLLRRRARRRDRRLVLDEGVTVPQKRTDEWMELEMGEFINEEGEDGEVCFSLMETK
                     GGNWKRGLIVQGIEIRLKKSG"
     gene            join(15841. .15901,16106. .16272,16375. .16439,16593. .16662,
                     16996. .17067,17165. .17368,18290. .18363,18462. .18545,
                     19079. .19166,19260. .19341,19675. .19748,19971. .20078,
                     20180. .20244,20814. .20927,21141. .21240,21337. .21390,
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                21469. .21825)
                /gene="OJ1293_E04.4-1"
     mRNA       join(15841. .15901,16106. .16272,16375. .16439,16593. .16662,
                16996. .17067,17165. .17368,18290. .18363,18462. .18545,
                19079. .19166,19260. .19341,19675. .19748,19971. .20078,
                20180. .20244,20814. .20927,21141. .21240,21337. .21390,
                21469. .21825)
                /gene="OJ1293_E04.4-1"
                /note="supported by full-length cDNA(s): AK100446"
     gene       15858. .20860
                /gene="OJ1293_E04.4-2"
     mRNA       join(<15858. .15901,16996. .17067,17165. .17368,18290. .18363,
                18462. .18545,19079. .20078,20814. .>20860)
                /gene="OJ1293_E04.4-2"
                /note="supported by full-length cDNA(s): AK066398"
     misc_feature 15858. .20860
                /gene="OJ1293_E04.4-2"
                /note="contains full-length cDNA(s): AK066398
                non-coding transcript
                probably inactive due to including stop codon(s) in CDS"
     CDS        join(16132. .16272,16375. .16439,16593. .16662,16996. .17067,
                17165. .17368,18290. .18363,18462. .18545,19079. .19166,
                19260. .19341,19675. .19748,19971. .20078,20180. .20244,
                20814. .20927,21141. .21240,21337. .21390,21469. .21564)
                /gene="OJ1293_E04.4-1"
                /note="contains EST(s): D22281(C10676),AU102120(C10676)
                contains full-length cDNA(s): AK100446,AK058270"
                /codon_start=1
                /product="glutathione reductase"
                /protein_id="BAD21653.1"
                /db_xref="GI:47847860"
                /translation="MARKMLKDEEVEVAVTDGGSYDYDLFVIGAGSGGVRGSRTSASF
                GAKVAICELPFHPISSDWQGGHGGTCVIRGCVPKKILVYGSSFRGEFEDAKNFGWEIN
                GDINFNWKRLLENKTQEIVRLNGVYQRILGNSGVTMIEGAGSLVDAHTVEVTKPDGSK
                QRYTAKHILIATGSRAQRVNIPGKELAITSDEALSLEELPKRAVILGGGYIAVEFASI
                WKGMGAHVDLFYRKELPLRGFDDEMRTVVASNLEGRGIRLHPGTNLSELSKTADGIKV
                VTDKGEEIIADVVLFATGRTPNSQRLNLEAAGVEVDNIGAIKVDDYSRTSVPNIWAVG
                DVTNRINLTPVALMEATCFSKTVFGGQPTKPDYRDVPCAVFSIPPLSVVGLSEQQALE
                EAKSDVLVYTSSFNPMKNSISKRQEKTVMKLVVDSETDKVLGASMCGPDAPEIIQGMA
                VALKCGATKATFDSTVGIHPSAAEEFVTMRTLTRRVSPSSKPKTNL"
     gene       complement(27410. .29382)
                /gene="OJ1293_E04.5"
     mRNA       complement(join(<27410. .27558,29301. .>29382))
                /gene="OJ1293_E04.5"
                /note="start and end point are not identified"
     CDS        complement(join(27410. .27558,29301. .29382))
                /gene="OJ1293_E04.5"
                /note="predicted by GENSCAN etc."
                /codon_start=1
                /product="hypothetical protein"
                /protein_id="BAD21654.1"
                /db_xref="GI:47847861"
                /translation="MELRSHRIYWPLYMLEMKWRGVRVRMRALSTCGTPTPAASAGQS
                LCAENRTTPTGNSSSHRGRLLHRRPRLSRQTD"
     gene       31777. .33484
                /gene="OJ1293_E04.6"
     mRNA       31777. .33484
                /gene="OJ1293_E04.6"
                /note="supported by full-length cDNA(s): AK107210"
     CDS        31845. .33236
                /gene="OJ1293_E04.6"
                /note="contains full-length cDNA(s): AK107210"
                /codon_start=1
                /product="putative fatty acid elongase 3-ketoacyl-CoA
                synthase 1"
                /protein_id="BAD21655.1"
                /db_xref="GI:47847862"
                /translation="MDLLPLVTLLLLAHAAAWVAWQAAARRRRATCYLLDYACHKPSD
                DRKVTTELAGAIIERNKRLGLPEYRFLLKVIVNSGIGEHTYSPRNVLDAREDCPTLRD
                ALDEMDDFFDDAVAAVLARAAVSPRDVDLLVINVGSFSPSPSLADRVVRRFGLRDDVM
                AYNLSGMGCSAGLVSVDLARNVMLTRPRTMALVLTSESCAPNWYTGTDKSMMLGNCLF
                RCGGAAALLTNDPAFRSRAKMELRCLVRAHIGAHDDAHAAAVHREDADGRLGVSLSKA
                LPKAAVRAFTENLQRLAPRILPAGELARFAARLLLRKLLRRKAAAGAAAKINFKTGVD
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                HFCLHPGGTAVIEAVRKSLGLDSYDVEPARMALHRWGNTSASSLWYVLSYMEAKRRLN
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                LPSQGQGGAFPFF"
     gene       35504. .35704
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     misc_feature 35504. .35704
                /gene="OJ1293_E04.7"
                /note="hypothetical ORF
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  Query Match             6.9%;  Score 113.4;  DB 8;  Length 118192;
  Best Local Similarity   77.1%;  Pred. No. 3.6e-21;
  Matches  138;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        517 AAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTT 576
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Db      64553 AACTGCAGGTTAACTTTGAAACTGCATTGAAACTTCGAGGAGGGCCTTCTTTAGTGTTT 64494

Qy        577 GCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATT 636
              || ||||| |||||||||||||| ||  | |||||||||||||||| |||  ||||||||
Db      64493 GCTCATTCCATGGGTAATAATGTGTTTCGCTACTTTCTGGAATGGTTGAAACTAGAAATC 64434

Qy        637 GCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG 695
              || || || ||||| |    ||||||||  | ||||| |||| || || || |||||
Db      64433 GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 64375
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RESULT 11
AP005691/c
LOCUS       AP005691               147123 bp    DNA     linear   PLN 02-JUN-2004
DEFINITION  Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
            BAC clone:OSJNBa0053L11.
ACCESSION   AP005691
VERSION     AP005691.3  GI:47848524
KEYWORDS    .
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Katayose,Y.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
            clone:OSJNBa0053L11
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 147123)
  AUTHORS   Sasaki,T., Matsumoto,T. and Katayose,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2002) Takuji Sasaki, National Institute of
            Agrobiological Sciences, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     On Jun 1, 2004 this sequence version replaced gi:38564216.
            Genes were predicted from the integrated results of the following:
            GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
            (http://www.softberry.com/), GeneMark.hmm
            (http://opal.biology.gatech.edu/GeneMark/), GlimmerM
            (http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM
            (http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
            (http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
            (http://globin.cse.psu.edu/html/docs/sim4.html), gap2
            (http://www.tigr.org/software/glimmerm/), BLASTN and BLASTX. The
            genomic sequence was searched against NCBI NonRedundant Protein
            database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
            sequence database at RGP or DDBJ. Protein homologies of the coding
            regions were searched against NCBI NonRedundant Protein database
            with BLASTP. ESTs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
            Full-length cDNAs represent the identified cDNA sequences using
            BLASTN with the corresponding DDBJ accession no.
            A gene with identity or significant homology to a protein is
            classified based on the protein name to indicate the homology level
            such as same name, 'putative-' and '-like protein'.  A gene without
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significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
The orientation of the sequence is from -21M13 to M13rev of the BAC clone. This sequence of OSJNBa0053L11 clone has an overlap with P0016F11 (DDBJ: AP005303) clone at 5' end and with OJ1293_E04 (DDBJ: AP004120) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES Location/Qualifiers

source 1. .147123
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
/clone="OSJNBa0053L11"

gene join(210. .282,431. .528,603. .662)
/gene="OSJNBa0053L11.1"

misc_feature join(210. .282,431. .528,603. .662)
/gene="OSJNBa0053L11.1"
/note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"

gene 2264. .3226
/gene="OSJNBa0053L11.2"

mRNA join(<2264. .2293,2852. .>3226)
/gene="OSJNBa0053L11.2"
/note="start and end point are not identified"

CDS join(2264. .2293,2852. .3226)
/gene="OSJNBa0053L11.2"
/note="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD22377.1"
/db_xref="GI:47848525"
/translation="MACHGDAYVSRRRGTNSARATESPPRRQASASARGSIASAATRD
SANAEGLRPLWLSASALSHGSVTSAITRNSYAVNVATSRGSPSLPPRATPPAARGYVA
SPPRRDTANPSTRHGGQTAAATRWPPLGSTCG"

gene 4436. .6725
/gene="OSJNBa0053L11.3"

mRNA join(4436. .4894,4982. .5164,5251. .5600,6156. .6617)
/gene="OSJNBa0053L11.3"
/note="supported by full-length cDNA(s): AK119257"

mRNA join(4438. .4894,4982. .5164,5251. .5600,6156. .6725)
/gene="OSJNBa0053L11.3"
/note="supported by full-length cDNA(s): AK063935"

CDS join(4586. .4894,4982. .5164,5251. .5600,6156. .6333)
/gene="OSJNBa0053L11.3"
/note="contains EST(s): AU182147(C63648),AU058044(C63006)
contains full-length cDNA(s): AK119257,AK063935"
/codon_start=1
/product="putative cinnamoyl CoA reductase"
/protein_id="BAD22378.1"
/db_xref="GI:47848526"
/translation="MSSNNSMEANNGDDEKKQEQVVCVTGAGGFIGSWVVKELLLRGY
RVRGTARDPRKNAHLLDLEGAKERLTLCRADVLDFASLRAAFAGCHGVFHIASPVSKD
PNLVPVAIEGTRNVMKAAADMGVRRVVFTSSYGAVHMNPNRSPDAVLDESCWSDPEFC
QREDIYCYAKMMAEKTATEEASRRRLQLAVVVPCVTVGPILQPSVNFSCHHVVRYLTG
AAATYPNAVAAYADVRDVARAHVLVYEHHGARGRYLCIGTVIHRAELLRMLKELFPQY
PVTSKCEDEGNQMVKPYKFSNQRLRDLGLEFTPLRKSLHEAIECLQRKGHLPVVTVAQ
QRACL"

gene complement(7826. .8435)
/gene="OSJNBa0053L11.4"

mRNA complement(join(<7826. .8214,8309. .>8435))
/gene="OSJNBa0053L11.4"
/note="start and end point are not identified"

CDS complement(join(7826. .8214,8309. .8435))
/gene="OSJNBa0053L11.4"
/note="similar to Oryza sativa chromosome 1, P0497A05.2"
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD22379.1"
/db_xref="GI:47848527"
/translation="MAAAGPSSSAPPRPGAGVATMVAGRRGDSAAGGRGALHGRRGAA
AVVADVVETKLATTAADCGSCRDAGPRHCSGCERRARDAFLHDASDPRVALHLRSASP
RPDLDVWRLVALASDGGGWTGVAVAVAVAMAMVADGGGCGSDGGGYRRCYLWRRWLKA
IIRLTVRHRRR"

gene 9814. .11214
/gene="OSJNBa0053L11.5"

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RDPELMAVAVDGTRNVMNAAADMGVRRVVFTSSYGAVHMNPNRSPDAVLDESCWSDPE
FCRQKDVSLLHMYCYAKTMAEMAATEEAAKRGLELAVVVPSMTMGPMLQRALNLSSTH
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PVVLP"

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predicted by GENSCAN
this category is not included in IRGSP standard"

gene 15304. .18533
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Qy        637 GCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG 695
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Db     126531 GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 126473


RESULT 12
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DEFINITION  Oryza sativa (japonica cultivar-group) chromosome 2 clone P0511E12,
            *** SEQUENCING IN PROGRESS ***.
ACCESSION   AP004882
VERSION     AP004882.1  GI:19698302
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
            clone:P0511E12
  JOURNAL   Published Only in Database (2002)
REFERENCE   2  (bases 1 to 158971)
  AUTHORS   Sasaki,T., Matsumoto,T. and Yamamoto,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
            Agrobiological Sciences, Rice Genome Research Program; Kannondai
            2-1-2, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
            Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT     NOTE: It currently consists of 1 contigs. Gaps between the contigs
            are represented as runs of N. The order of the pieces is believed
            to be correct as given, however the sizes of the gaps between them
            are based on estimates that have provided by the submitter. This
            sequence will be replaced by the finished sequence as soon as it is
            available and the accession number will be preserved.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
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Db      58178 GCTCATTCCATGGGTAATAATGTGTTTCGCTACTTTCTGGAATGGTTGAAACTAGAAATC 58119

Qy        637 GCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGG 695
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Db      58118 GCTCCCAAGCATTACATCCGATGGCTTGACGAACATATACATGCATACTTTGCAGTTGG 58060


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DEFINITION  Novel class enzyme in biosynthesis pathway of triacrylglycerol
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ACCESSION   BD271624
VERSION     BD271624.1  GI:33081392
KEYWORDS    JP 2002541783-A/9.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 709)
  AUTHORS   Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
  TITLE     Novel class enzyme in biosynthesis pathway of triacrylglycerol
            production and recombinant DNA molecule encoding the enzyme
  JOURNAL   Patent: JP 2002541783-A 9 10-DEC-2002;
            BASF PLANT SCIENCE GMBH
COMMENT     OS   Lycopersicon esculentum (tomato)
            PN   JP 2002541783-A/9
            PD   10-DEC-2002
            PF   28-MAR-2000 JP 2000609586
            PR   01-APR-1999 EP   99106656.4,10-JUN-1999 EP   99111321.8 PR
            07-FEB-2000 US    60/180687
            PI   ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI
            ,HANS RONNE,STEN STYMNE
            PC   C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC
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            CC          production
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DEFINITION  Novel class enzyme in biosynthesis pathway of triacrylglycerol
            production and recombinant DNA molecule encoding the enzyme.
ACCESSION   BD271634
VERSION     BD271634.1  GI:33081402
KEYWORDS    JP 2002541783-A/19.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 709)
  AUTHORS   Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
  TITLE     Novel class enzyme in biosynthesis pathway of triacrylglycerol
            production and recombinant DNA molecule encoding the enzyme
  JOURNAL   Patent: JP 2002541783-A 19 10-DEC-2002;
            BASF PLANT SCIENCE GMBH
COMMENT     OS   Lycopersicon esculentum (tomato)
            PN   JP 2002541783-A/19
            PD   10-DEC-2002
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            PR   01-APR-1999 EP   99106656.4,10-JUN-1999 EP   99111321.8 PR
            07-FEB-2000 US    60/180687
            PI   ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI
            ,HANS RONNE,STEN STYMNE
            PC   C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC
            (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
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            of triacrylglycerol
            CC           production
            CC   and recombinant DNA molecule encoding the enzyme FH   Key
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Qy       1486 CATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAA 1545
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RESULT 15
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VERSION     AX037588.1  GI:11227007
KEYWORDS    .
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  ORGANISM  Lycopersicon esculentum
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            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1
  AUTHORS   Banas,A., Stahl,U., Stymne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
  TITLE     A new class of enzymes in the biosynthetic pathway for the
            production of triacylglycerol and recombinant dna molecules
            encoding these enzymes
  JOURNAL   Patent: WO 0060095-A 12 12-OCT-2000;
            BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
            STYMNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
            ANDERS (SE)
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SUMMARIES

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c	16	34.4	2.1	511	4	US-09-620-405B-443	Sequence 443, App
c	17	34.4	2.1	511	4	US-09-433-826B-443	Sequence 443, App
c	18	34.4	2.1	511	4	US-09-604-287A-443	Sequence 443, App
c	19	34.4	2.1	511	4	US-09-834-759-443	Sequence 443, App
c	20	34.4	2.1	511	4	US-09-590-751A-443	Sequence 443, App
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c	24	33.6	2.0	270	4	US-09-248-796A-3827	Sequence 3827, Ap
c	25	33.6	2.0	749	4	US-09-673-395A-48	Sequence 48, Appl
	26	33.4	2.0	14273	4	US-08-961-527-40	Sequence 40, Appl
c	27	33.2	2.0	957	4	US-09-583-110-991	Sequence 991, App
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c	35	32.4	2.0	3477	4	US-09-462-720-3	Sequence 3, Appli
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c	42	32	2.0	543	6	5273901-6	Patent No. 5273901
c	43	32	2.0	586	3	US-09-385-982-139	Sequence 139, App
c	44	32	2.0	675	4	US-09-248-796A-3828	Sequence 3828, Ap
	45	32	2.0	1638	4	US-09-134-000C-140	Sequence 140, App

ALIGNMENTS

RESULT 1
US-09-248-796A-1147
; Sequence 1147, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1147
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (341)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-248-796A-1147

Query Match 2.9%; Score 47.2; DB 4; Length 2106;
Best Local Similarity 47.8%; Pred. No. 6e-05;
Matches 173; Conservative 0; Mismatches 183; Indels 6; Gaps 1;

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Qy        395 TCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCG 454
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Db        881 TTTGGAATAAAATTTTACAAAACTTAGCTGTGATTGGTTATGGACCCAATAATATGATTA 940

Qy        455 CTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTC 514
              ||   | || || ||||||||  |    |   | || ||  |  | ||    || |||
Db        941 GTGCCTCGTATGACTGGAGATTAACTTATATTGATTTAGAGAAAAGAGATGGATATTTTT 1000

Qy        515 ACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTATAGTAT 574
              ||  | ||        |||||| ||    | || |    ||        ||  || ||
Db       1001 CTAAATTGAAAGCACAAGTTGAAATTGTCAAACAATTGACAGGTAAAAAATCAGTATTAG 1060

Qy        575 TTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTG------AGGC 628
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Db       1061 TGGGCCATTCAATGGGTTCACAAATTATTTATTATTTTTTGAAATGGGTTGAAGCCAAAG 1120

Qy        629 TAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCG 688
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Db       1121 GAGAATATTATGGTAACGGAGGACCTAATTGGGTCGAAGATTACGTTGAAGCATTTGTTA 1180
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Qy        689 CTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCTCTCTGGTGTAA 748
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Db       1181 ATATTAGTGGATCTTCTTTGGGTACACCAAAGGCTATCCCAGCATTAATTTCTGGTGAAA 1240

Qy        749 CG 750
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Db       1241 TG 1242


RESULT 2
US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
;  APPLICANT: Bult et al.
;  TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6503729
;  TITLE OF INVENTION:  jannaschii
;  FILE REFERENCE: PB275
;  CURRENT APPLICATION NUMBER: US/08/916,421B
;  CURRENT FILING DATE:  1997-08-22
;  PRIOR APPLICATION NUMBER: US 60/024,428
;  PRIOR FILING DATE: 1996-08-22
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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;   TYPE: DNA
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;   OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

  Query Match             2.5%;  Score 40.6;  DB 4;  Length 1664976;
  Best Local Similarity   47.8%;  Pred. No. 1.2;
  Matches  118;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        330 TGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTC 389
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Qy        390 TACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAAT 449
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Qy        450 TGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTA 509
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Qy        510 CTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTAT 569
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Db    1220397 ATTTAATAAGCTTTACTATCTTTATGCAAATGCAAAATAATTCCTTAATTTTCCTATTTT 1220456

Qy        570 AGTATTT 576
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Db    1220457 CGTAATT 1220463


RESULT 3
US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
;  APPLICANT: Bult et al.
;  TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
; Patent No. 6797466
;  TITLE OF INVENTION:  jannaschii
;  FILE REFERENCE: PB275C1
;  CURRENT APPLICATION NUMBER: US/09/692,570
;  CURRENT FILING DATE:  2003-01-14
;  PRIOR APPLICATION NUMBER: US 60/024,428
;  PRIOR FILING DATE: 1996-08-22
;  PRIOR APPLICATION NUMBER: US 08/916,421
;  PRIOR FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: Methanococcus jannaschii
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  Best Local Similarity   47.8%;  Pred. No. 1.2;
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Qy        330 TGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTC 389
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Qy        390 TACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAAT 449
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Db    1220277 GATAAAATGTAATGGATGTTATAAAAGAGATGTTGAGATTTGCAAAGAAGTATGTCCAAC 1220336

Qy        450 TGTCGCTGTTCCATACGATTGGAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTA 509
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Db    1220337 AGGAGCTATTAACAACCTTGAAGAAATATTAAATAATAAAATACAAAATACAGTGAATAA 1220396

Qy        510 CTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAAAACTCCGTGGCGGCCCTTCTAT 569
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Db    1220397 ATTTAATAAGCTTTACTATCTTTATGCAAATGCAAAATAATTCCTTAATTTTCCTATTTT 1220456

Qy        570 AGTATTT 576
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Db    1220457 CGTAATT 1220463


RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-Fls
US-08-232-463-14

  Query Match             2.4%;  Score 38.6;  DB 1;  Length 7218;
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  Matches   11;  Conservative  190;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        486 CAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTT 545
              ||  | |   |||| ||   |:: ::::: :   :::   ::  :::::    :: ::::
Db       1046 CAGGTCGAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1105

Qy        546 AAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAG 605
              :::: :  :  ::::::: :  : ::: ::: ::: :   :   :  : :::::
Db       1106 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1165

Qy        606 ATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGA 665
              : ::::::    :  ::    ::     :: : ::    : :: :::    :  :::
Db       1166 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1225

Qy        666 TCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAAT 725
              ::  : : ::: : ::: :::: :: ::    :::::::::::  :::: ::    :  :
Db       1226 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1285

Qy        726 CAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGTT 785
              :  ::: ::::::::  : :  : :::  ::::::: :::::       :: :::  ::
Db       1286 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1345

Qy        786 GTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTC 830
              :: :::  ::::::: : :: :: :: :  ::: : :: :::::
Db       1346 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1390


RESULT 5
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
;  APPLICANT: The University of British Columbia
;  TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
;  FILE REFERENCE: 4810-58741
;  CURRENT APPLICATION NUMBER: US/09/806,708B
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/147,133
;  PRIOR FILING DATE: 1999-08-04
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
;   LENGTH: 1141
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (1)..(1141)
;   OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

  Query Match             2.3%;  Score 38.2;  DB 4;  Length 1141;
  Best Local Similarity   9.6%;  Pred. No. 0.045;
  Matches   73;  Conservative  280;  Mismatches  405;  Indels    3;  Gaps    1;

Qy        488 AATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGCTTTAA 547
              :::|:  :: ::        |::::::| :: :  ::  |          ||    |::|
Db        884 RHHTRTCRRTKYNNNNNNARTVYWYHHAARRWMNAWWTRTNNNNNNNNNNACRNTRTWWA 825

Qy        548 AACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGAT 607
              : ::              |: : ||   :: :          :: :    : : |: |
Db        824 BWKHSWCNNNNNNNNNNNNNNTWCHYTTANABBCYRANNNNAAARMARTCNNYMHAAVTT 765

Qy        608 ACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATC 667
              :|::|:: ::   ::::                : :       :          ::|::
Db        764 THTDWCYKTWMNTWYWDMMTTMBTTTTRNMTTSTNMTNNNNNNMWACTNNNNNNMWKAYY 705

Qy        668 AGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGGCAATCA 727
              |      : |::  |:|  |   |: :::      | :::||:::::|| |
Db        704 AHATNNWGCWWNNTDARRTNNTTVMRRRWMTNTKTRWYSTTRRHHYTGATNNNNNNNNNN 645

Qy        728 AATCTACTCTCTCTGGTGTAACG---TTTGGCCTTCCTGTTTCTGAGGGAACTGCTCGGT 784
              : ||||     :: : |   |  ::: :   | |:    |:: :: :  :::
Db        644 NNNNNNSCCTCTRMMTMRWTMKGDGMTVRKKVKWRDTTCTYVDVWADSWVWWYANWMRCR 585

Qy        785 TGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGCAAGG 844
              ::|:       ::: :    ::   :::: :   : :: ::||   ::   : :::: |
Db        584 DVTYTRNNTYCKSYAHSYWYWSNNAMWYRRYSARNWSSMARWTTRNNWWMSGBVRMRWAG 525

Qy        845 GTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTAT 904
              : ::    |      :   ::  :|:|: ::    :::::   :: :::     :|
Db        524 TMWWRHWNNNNTDTRYYWWWKRWARBTTTVYDSMCNAKSMWRGNNWRAMKMWWAANNDAG 465

Qy        905 ACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTA 964
              |: : | :     : :::|:::  :|:|::|        :  : :   ::::|:::::|
Db        464 AMDHWTYWMGNNTMWMRRAWKMMNMAWCRRAYCCNNNNNRACVWHKHKMWRWTWKYMWKA 405

Qy        965 ACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGG 1024
              ||       | ::    ::: ::   |: : :   :: : : ::: :::        :::
Db        404 ACNNNNBKAMYMRVAWMMYSRDTTNTDWMMWTSDWBWHWYTVDYTMMRAWNNNNNNNWRB 345

Qy       1025 AATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACTCTTT 1084
```

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Db        344 CKTTSWMWWMDHMNTHCTYGNNTWGSAYBMAAMSMWAAGASNBVTYNWCWRMTYMGKTMT 285

Qy       1085 TCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAGAAGT 1144

Db        284 NNNNNNKAWYYRTKTVAWCNNRYYYDTAVWTBKRNYKYCYAYBWYYBMYMGKHHWBWWRR 225

Qy       1145 TGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATAAAAA 1204

Db        224 ABHRSWNMWWVKCRNKYMVSWHYHAMRYBKWABAVGCNNNWKDRMAHHHWCATNNNMMWW 165

Qy       1205 ATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTT 1245

Db        164 WYAYMHHMHKKGKAAWTNNKTABRDDHBAHVKTYWYWRYDY 124


RESULT 6
US-09-621-976-2439/c
; Sequence 2439, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2439
;   LENGTH: 581
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 146..310
US-09-621-976-2439

  Query Match             2.2%;  Score 36.6;  DB 4;  Length 581;
  Best Local Similarity   47.9%;  Pred. No. 0.097;
  Matches  105;  Conservative    0;  Mismatches  114;  Indels    0;  Gaps    0;

Qy        596 ATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGA 655

Db        395 AAGTCTTCAGGTGCTCCTTCCTATAGCAGATGGTCCAGTTCACAGCCACATCAGGATAAA 336

Qy        656 AGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTG 715

Db        335 TATAGGCTGAATCTCTTTTCCATTATAAATTCTCCCTTAGTAATCCTTTTGTGATTTTTG 276

Qy        716 TTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAA 775

Db        275 TATTGGAAATTGAGGGTTGGCTAATTGAAGTCAGATGTTCAGTGCAGAGTGTTGCAGCGT 216

Qy        776 CTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGT 814

Db        215 ATCCCAATTTGTTGCCTTGTTTCTCTGTTCTCTCTTTGT 177


RESULT 7
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2813
;   LENGTH: 832
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 235..399
US-09-621-976-2813

  Query Match             2.2%;  Score 35.6;  DB 4;  Length 832;
  Best Local Similarity   11.5%;  Pred. No. 0.27;
  Matches   37;  Conservative  150;  Mismatches  134;  Indels    1;  Gaps    1;

Qy        363 TCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGT 422

Db         26 WMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWRYAMWGTYKKKAMCRTKTKKKKKKG 85

Qy        423 TGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACC 482

Db         86 YMWMWYWGWRRSYMAMWTRTWTGYAYYRSMMYWWRYRCWKKKAYYRKTTCYSSKGWTWWK 145

Qy        483 AACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACTGC 542

Db        146 RW-KKAWTTWWWKKTYYWAATRYWWMMCWTKRWRASWWYCWWWGKARKWSTWRKSRSYAS 204

Qy        543 TTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTT 602

Db        205 ARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYKSM 264

Qy        603 CAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCT 662

Db        265 WMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWARMYRYSTGT 324

Qy        663 TGATCAGCATATCCATGCTTAT 684

Db        325 RASMWWRRWYYTMMMKWWKYAW 346


RESULT 8
US-08-809-254A-4
; Sequence 4, Application US/08809254A
; Patent No. 6660852
; GENERAL INFORMATION:
;  APPLICANT: KESHI ET AL
;  TITLE OF INVENTION: PROBE FOR DIAGNOSING INFECTIOUS DISEASES
;  FILE REFERENCE: 19036/33767
;  CURRENT APPLICATION NUMBER: US/08/809,254A
;  CURRENT FILING DATE:  1997-05-16
;  PRIOR APPLICATION NUMBER: PCT/JP95/02036
;  PRIOR FILING DATE: 1995-10-02
;  PRIOR APPLICATION NUMBER: JP 236348
;  PRIOR FILING DATE: 1994-09-30
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 5829
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic probe
US-08-809-254A-4

  Query Match             2.1%;  Score 35;  DB 4;  Length 5829;
  Best Local Similarity   49.2%;  Pred. No. 1.7;
  Matches   92;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        642 AAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCC 701

Db       3443 AACGCATACTATTAAGCTTTTTCAAGACCTAATAATATGCGCTGTTCTGATTTGAAAGAC 3502

Qy        702 TCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCC 761
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Db       3503 ATTCCATTATTATTTTACTGTAATCAAGCCATCTGGCTCTACTGTGAATTCTGGCTTGTC 3562

Qy        762 TGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTAT 821
              ||    ||      ||| |  |  || || | |  || || ||||  |    ||| | |
Db       3563 TGCCAGTGTTCCGTCTGGTTTGAGGTAGTACCAGCCTGTTCCGTCCGCTGACTGGATAAA 3622

Qy        822 GCCATTT 828
              | |||||
Db       3623 GGCATTT 3629


RESULT 9
US-08-961-527-41/c
; Sequence 41, Application US/08961527
; Patent No. 6420135
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Streptococcus pneumoniae Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  391
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/961,527
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brookes, A. Anders
;      REGISTRATION NUMBER:  36,373
;      REFERENCE/DOCKET NUMBER:  PB340P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9828 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-961-527-41

  Query Match             2.1%;  Score 35;  DB 4;  Length 9828;
  Best Local Similarity   49.2%;  Pred. No. 2.5;
  Matches   92;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        642 AAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCC 701
              ||  |||  | | |||    || |  | |  ||         | |      || ||    |
Db       4114 AACGCATACTATTAAGCTTTTTCAAGACCTAATAATATGCGCTGTTCTGATTTGAAAGAC 4055

Qy        702 TCTTCTTGGTTCTGTTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCC 761
                | | |  || | ||   | ||||||  |  ||  ||||  ||| |  | ||||  |  |
Db       4054 ATTCCATTATTATTTTACTGTAATCAAGCCATCTGGCTCTACTGTGAATTCTGGCTTGTC 3995

Qy        762 TGTTTCTGAGGGAACTGCTCGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTAT 821
              ||    ||      ||| |  |  || || | |  || || ||||  |    ||| | |
Db       3994 TGCCAGTGTTCCGTCTGGTTTGAGGTAGTACCAGCCTGTTCCGTCCGCTGACTGGATAAA 3935

Qy        822 GCCATTT 828
              | |||||
Db       3934 GGCATTT 3928


RESULT 10
US-09-710-279-2485
; Sequence 2485, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2485
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2485

  Query Match             2.1%;  Score 34.8;  DB 4;  Length 462;
  Best Local Similarity   50.6%;  Pred. No. 0.34;
  Matches   84;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy        865 CATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAA 924
              ||| ||| | |      |||  |||  | || |    | |||| | |    |    | ||
Db        148 CATATTTATCGCCTGCCTGTGAAGGCAAATCAATATGAATACAAATTACTTACGCAACAA 207

Qy        925 TATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTCCTTCCACT 984
              | ||||| | | |    |  | |  |   ||  |||  | |  ||||||  |  ||||
Db        208 TCTCAATTAGACTCAAGAGTAAGACTAAATGATTATATAGAAACAGAAATTATTAACACT 267

Qy        985 AGCGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTG 1030
              |   ||| |||| |   | || | |  | ||| |      | || ||
Db        268 ATGATTAAAGAATCGTATATACTAATAAAGACGACACCAGGATTTG 313


RESULT 11
US-09-134-001C-1521
; Sequence 1521, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1521
;   LENGTH: 477
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1521

  Query Match             2.1%;  Score 34.8;  DB 3;  Length 477;
  Best Local Similarity   50.6%;  Pred. No. 0.35;
  Matches   84;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy        865 CATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAA 924
              ||| ||| | |      |||  |||  | || |    | |||| | |    |    | ||
Db        163 CATATTTATCGCCTGCCTGTGAAGGCAAATCAATATGAATACAAATTACTTACGCAACAA 222

Qy        925 TATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTCCTTCCACT 984
              | ||||| | | |    |  | |  |   ||  |||  | |  ||||||  |  ||||
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Db        223 TCTCAATTAGACTCAAGAGTAAGACTAAATGATTATATAGAAACAGAAATTATTAACACT 282

Qy        985 AGCGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTG 1030
              |   ||| |||| |   | || | |  | ||| |     | || ||
Db        283 ATGATTAAAGAATCGTATATACTAATAAAGACGACACCAGGATTTG 328


RESULT 12
US-09-710-279-4015/c
; Sequence 4015, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4015
;   LENGTH: 3926
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4015

  Query Match             2.1%;  Score 34.8;  DB 4;  Length 3926;
  Best Local Similarity   50.6%;  Pred. No. 1.5;
  Matches   84;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy         865 CATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGCGTATACCACTGTGATGAAGAGGAA 924
               ||| ||| | |     |||  |||  | || |    | |||| | |    |   |  ||
Db        3455 CATATTTATCGCCTGCCTGTGAAGGCAAATCAATATGAATACAAATTACTTACGCAACAA 3396

Qy         925 TATCAATCAAAATATTCTGGCTGGCCGACAAATATTATTAACATTGAAATTCCTTCCACT 984
               | ||||| | | |     |   | |  |   ||  |||  | |  ||||||  |  ||||
Db        3395 TCTCAATTAGACTCAAGAGTAAGACTAAATGATTATATAGAAACAGAAATTATTAACACT 3336

Qy         985 AGCGTTACAGAAACAGCTCTAGTCAACATGACCAGCATGGAATGTG 1030
               |   ||| |||| |   | || | |  | ||| |     | || ||
Db        3335 ATGATTAAAGAATCGTATATACTAATAAAGACGACACCAGGATTTG 3290


RESULT 13
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.1%;  Score 34.8;  DB 1;  Length 7218;
  Best Local Similarity   7.6%;  Pred. No. 2.4;
  Matches   33;  Conservative  203;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        1200 AAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGC 1259
               |||||  | || | |      |  ||  | | |||   |   | || | | |  | | |
Db        1506 AAAAACGGCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGA 1447

Qy        1260 CCCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGA 1319
               |  ||| | :   :   :: ::  :::  :  : ::: :  :   : ::::  ::
Db        1446 AGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1387

Qy        1320 AGGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGG 1379
               :::       : :  ::::   ::::  : ::  :: ::::: :  :::   : ::  ::
Db        1386 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1327

Qy        1380 GGATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGT 1439
               ::: :::: :: :    :  :   :        :: : :::::  ::   :::   ::::
Db        1326 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1267

Qy        1440 TAACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAA 1499
                :: : :: :: ::      ::  :::: : :: ::::: :: : : : : :::: :::
Db        1266 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1207

Qy        1500 TGTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAA 1559
                :  ::  : ::: : :::  ::: :  : ::  :: : : :: ::::: :  :::::  ::
Db        1206 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1147

Qy        1560 GTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGA 1619
               : : : ::      : :::::    ::::: :    ::::::::::::  : ::   ::::
Db        1146 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1087

Qy        1620 GCTTGATAAAAGTGGG 1635
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Db        1086 RRRRRRRRRRRRRRRR 1071


RESULT 14
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
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;  SOFTWARE: Patent.pm
; SEQ ID NO 2813
;   LENGTH: 832
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 235..399
US-09-621-976-2813

  Query Match             2.1%;  Score 34.6;  DB 4;  Length 832;
  Best Local Similarity   9.4%;  Pred. No. 0.6;
  Matches   34;  Conservative  164;  Mismatches  163;  Indels    0;  Gaps    0;

Qy        960 TATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAG 1019
              | :: :  |:  : |:  | : ::: : : : ::    :|    :::: :  :: :  :
Db        363 TYYWTWWKTWWYWTTYTWTRMWWMKKKARRWYYWWKSTYACASRYRKYTWGWWWYMWKRM 304

Qy       1020 CATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGAC 1079
              : |:   :   :|| :   :|  :|  :   : :|  :  :  :|::    :  ::|: :
Db        303 MSTRWYCYMCWKCCMYRGRRCAWYTMARGRMWSYAWGKWKSMRSAMSMCTRMYYKKGSTY 244

Qy       1080 TCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAA 1139
              :  : ||| : :: :  : ::   | :: ::| :: :  : ::   ::|::::   :::
Db        243 WTMKCTCATWCYWYWKYWKRMWSKTCWSGSRGGYMTSYTSTRSYSMYWASWMYTMCWWWG 184

Qy       1140 GAAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTAT 1199
              ::::|: ::   ::::::    ::    :::   |:   ::  :  :::|| :: : : ::
Db        183 RWWSTYWYMAWGKKWWRYATTWRRAMMWWWAAWTMMWYMWWAWCMSSRGAAMYRRTMMMW 124

Qy       1200 AAAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGC 1259
                : :: :: :  |:||:|:|:: ::::::   : :::|: :      :  | ::
Db        123 GYRYWWRKKSYRRTRCAWAYAWKTKRSYYWCWRWKWKRCMMMMMMAMAYGKTMMMRACWK 64

Qy       1260 CCCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGA 1319
                ::: :   :::: :|: ::: :::: :::::: : :  ::::|:     ||::: :
Db         63 TRYWRWWAWAMWRMWWTMMMMYYWYWRAMKRRWMWRKWRSWSWMWMAWGMTRWAARMWWR 4

Qy       1320 A 1320
              :
Db          3 W 3
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RESULT 15
US-09-389-681-443/c
; Sequence 443, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C3
;  CURRENT APPLICATION NUMBER: US/09/389,681A
;  CURRENT FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 443
;   LENGTH: 511
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(511)
;   OTHER INFORMATION: n = A,T,C or G
US-09-389-681-443

  Query Match             2.1%;  Score 34.4;  DB 4;  Length 511;
  Best Local Similarity   46.9%;  Pred. No. 0.5;
  Matches  107;  Conservative    0;  Mismatches  121;  Indels    0;  Gaps    0;
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Qy        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020
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Db        233 ATGATCTTGGCACTGTCAGACACGGAGCAGAGACTAGAAGCCCAAGTCAACAGGAACACC 174

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
              ||  |  |   |||  |||| | || | ||    |||       | |         |
Db        173 ATCTATAGCACCCTGGTCACCTGTGTGACATTTGTGGCCACACTGCCTGTGCTCTACATG 114

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
              || |||||||| |   ||  |  | |||   |   || |  ||   ||  || |
Db        113 CTATTCAAAGCCAGCTAACCCCTGGCCCCTCCTCCAGAGGGTCTGAGGCAATAGCTGTGA 54

Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAG 1188
              | || |  | | |  ||   |  |  |||      ||  | |||| |
Db         53 ATGTGGATTTAAGTAGAGAATCGTAGCAATGAAGCGAGCCTTTGGGGG 6
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Job time : 162 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 8, 2004, 22:55:47 ; Search time 852 Seconds
(without alignments)
10370.111 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

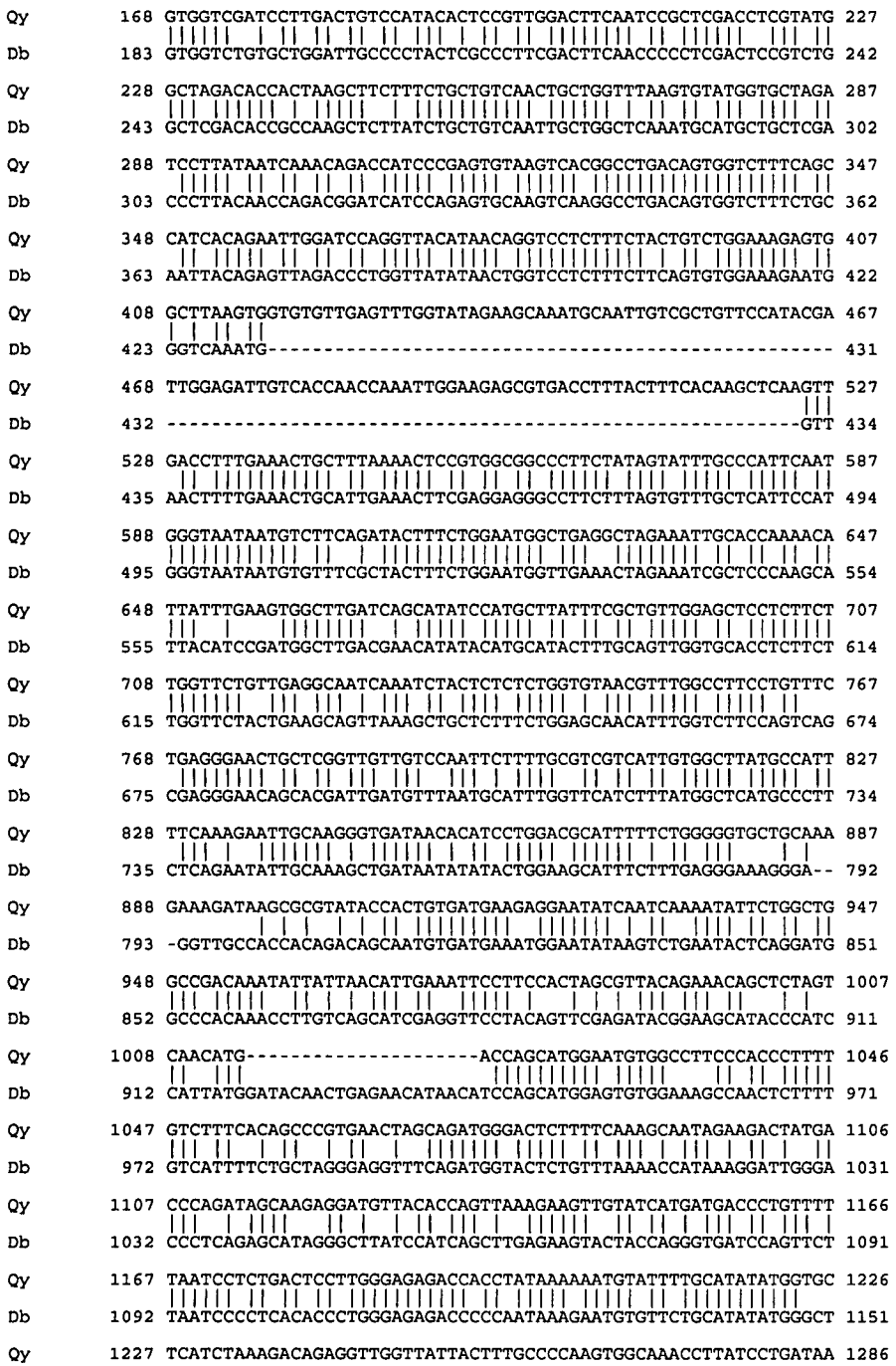
	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	591.8	36.1	1719	17	US-10-437-963-76086	Sequence 76086, A
	2	252.6	15.4	1760	16	US-10-424-599-16008	Sequence 16008, A
	3	215.8	13.2	528	16	US-10-424-599-134518	Sequence 134518,
	4	193	11.8	924	18	US-10-425-115-137717	Sequence 137717,
	5	187.8	11.4	848	18	US-10-425-115-93907	Sequence 93907, A
	6	173.8	10.6	1383	18	US-10-425-115-93909	Sequence 93909, A
	7	120.8	7.4	1433	16	US-10-424-599-17331	Sequence 17331, A
	8	72.2	4.4	380	16	US-10-424-599-57573	Sequence 57573, A
	9	56.6	3.4	369	18	US-10-425-115-57116	Sequence 57116, A
	10	51	3.1	962	18	US-10-425-115-61794	Sequence 61794, A
	11	44	2.7	374	18	US-10-425-115-93908	Sequence 93908, A
c	12	38.8	2.4	486	15	US-10-465-217-13	Sequence 13, Appl
	13	38	2.3	1545	16	US-10-424-599-56537	Sequence 56537, A
	14	37.6	2.3	394	16	US-10-242-535A-23539	Sequence 23539, A
	15	37.6	2.3	394	16	US-10-085-783A-23539	Sequence 23539, A
	16	37.6	2.3	473	14	US-10-060-036-226	Sequence 226, App
	17	37.6	2.3	3737	15	US-10-240-965-140	Sequence 140, App
	18	36.6	2.2	1939	18	US-10-425-115-31256	Sequence 31256, A
c	19	36.2	2.2	3325	17	US-10-437-963-65323	Sequence 65323, A
	20	36	2.2	735	17	US-10-437-963-38267	Sequence 38267, A
c	21	36	2.2	2395	17	US-10-437-963-38278	Sequence 38278, A
	22	36	2.2	2433	15	US-10-321-802-21	Sequence 21, Appl
	23	35.6	2.2	2356	9	US-09-822-830A-324	Sequence 324, App
	24	35.6	2.2	4089	9	US-09-764-877-3884	Sequence 3884, Ap
	25	35.6	2.2	4089	16	US-10-242-515-3884	Sequence 3884, Ap
c	26	35.6	2.2	17703	16	US-10-257-166-34	Sequence 34, Appl
c	27	35.6	2.2	43680	15	US-10-257-378-3	Sequence 3, Appli
	28	35.4	2.2	160	16	US-10-242-535A-42853	Sequence 42853, A
	29	35.4	2.2	160	16	US-10-085-783A-42853	Sequence 42853, A
c	30	35.4	2.2	416	13	US-10-079-623-57	Sequence 57, Appl
c	31	35.4	2.2	599	16	US-10-338-110-117	Sequence 117, App
c	32	35.4	2.2	1119	17	US-10-767-701-11611	Sequence 11611, A
c	33	35.4	2.2	3172	18	US-10-739-930-1299	Sequence 1299, Ap
c	34	35.2	2.1	2456	17	US-10-437-963-61433	Sequence 61433, A
	35	35.2	2.1	7219	17	US-10-437-963-13743	Sequence 13743, A
c	36	35	2.1	9828	8	US-08-961-527-41	Sequence 41, Appl
c	37	35	2.1	9828	16	US-10-158-844-41	Sequence 41, Appl
c	38	35	2.1	2256646	17	US-10-470-565-1	Sequence 1, Appli
	39	34.8	2.1	507	16	US-10-282-122A-10934	Sequence 10934, A
c	40	34.8	2.1	560	15	US-10-125-968-962	Sequence 962, App
c	41	34.8	2.1	8711	16	US-10-221-714A-424	Sequence 424, App
c	42	34.6	2.1	916	14	US-10-184-644-78	Sequence 78, Appl
c	43	34.6	2.1	916	14	US-10-184-634-78	Sequence 78, Appl
c	44	34.6	2.1	26112	10	US-09-764-872-627	Sequence 627, App
c	45	34.4	2.1	511	9	US-09-604-287A-443	Sequence 443, App

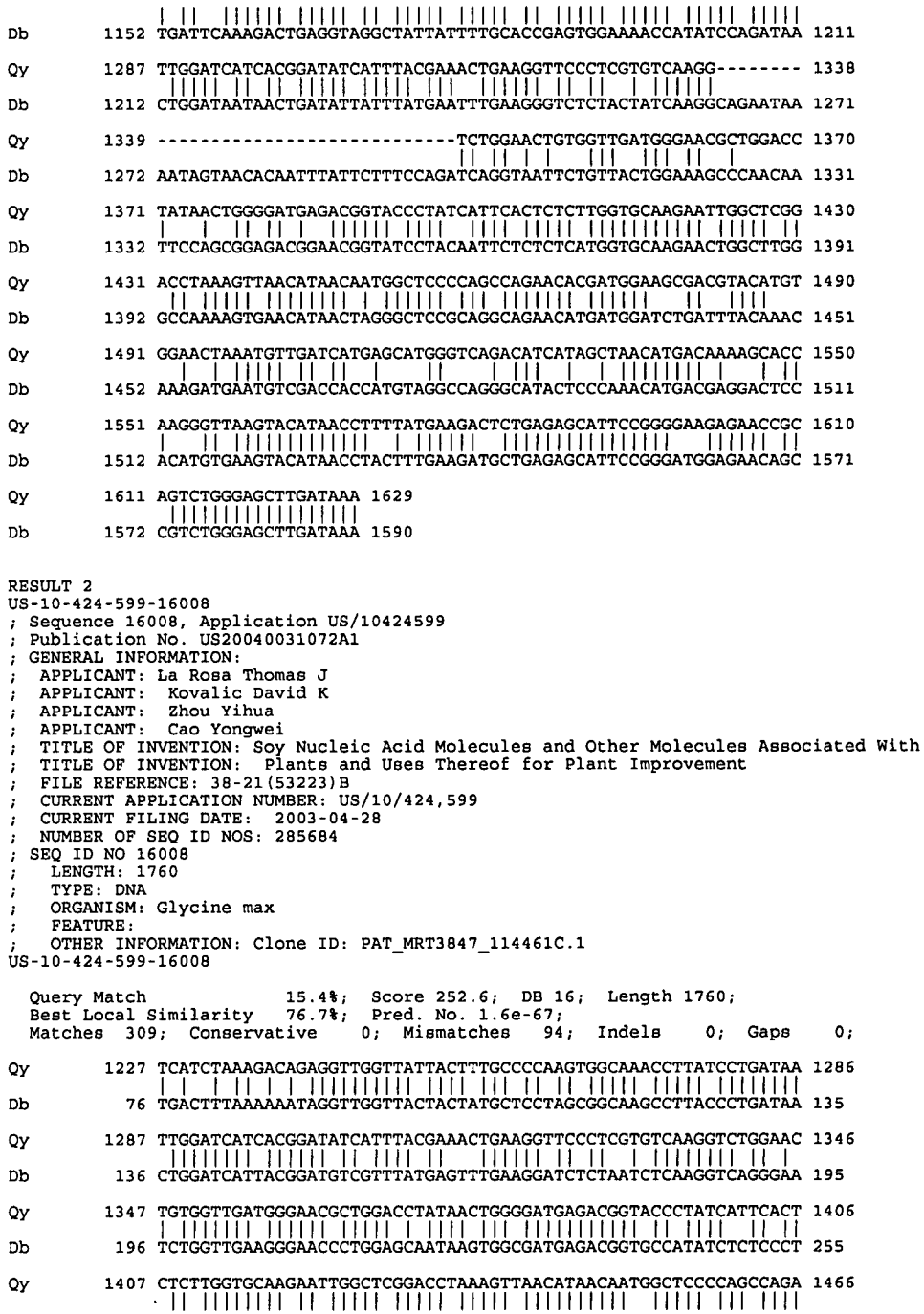
ALIGNMENTS

RESULT 1
US-10-437-963-76086
; Sequence 76086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 76086
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76111C.1
US-10-437-963-76086

Query Match 36.1%; Score 591.8; DB 17; Length 1719;
Best Local Similarity 65.2%; Pred. No. 9.2e-174;
Matches 1029; Conservative 0; Mismatches 382; Indels 168; Gaps 4;

Qy 108 CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGC 167
Db 123 CGACTACCGGAAGCTCTCGGGGATAATAATCCCCGGGTTCGCGTCGACGCAGCTGCGCGC 182





RESULT 2
US-10-424-599-16008
; Sequence 16008, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 16008
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114461C.1
US-10-424-599-16008

Query Match 15.4%; Score 252.6; DB 16; Length 1760;
Best Local Similarity 76.7%; Pred. No. 1.6e-67;
Matches 309; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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Db        256 TTCCTGGTGCAAAAACTGGCTTGGACCGAAAGTGAACATAACAAAAGCTCCACAGTCAGA 315

Qy       1467 ACACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGGTCAGACAT 1526
              || |||||     || |||||  |  || | ||||| || ||| | ||||     ||| ||
Db        316 GCATGATGGCTCAGATGTACAAATTAAATTGAATGTGGAACATCACCATGAAGAAGATAT 375

Qy       1527 CATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAAGACTCTGA 1586
              |  |  | |||||||||| | |||||||||| ||||| ||||| | |||||||||| |||||
Db        376 CGTTCCAAACATGACAAGATCACCAAGGGTGAAGTATATAACATATTATGAAGATTCTGA 435

Qy       1587 GAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAA 1629
              ||  |||| || ||||| || ||||| ||||||||||||||||
Db        436 AAGTCTTCCTGGAAAGAGGACAGCAGTTTGGGAGCTTGATAAA 478


RESULT 3
US-10-424-599-134518
; Sequence 134518, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 134518
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_9247C.1
US-10-424-599-134518

  Query Match            13.2%;  Score 215.8;  DB 16;  Length 528;
  Best Local Similarity  80.7%;  Pred. No. 2.6e-56;
  Matches  264;  Conservative    0;  Mismatches   62;  Indels    1;  Gaps    1;

Qy        108 CGACTACTCGAAGCTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGC 167
              |||||||||||||||| || || || || || || || || ||||| || ||||| |||||
Db        202 CGACTACTCGAAGCTCTCCGGCATTATAATCCCCGGCTTCGCGTCCACTCAGCTCCGAGC 261

Qy        168 GTGGTCGATCCTTGACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATG 227
              |||||  || || |||||||| ||| ||||| | || ||||| || |||||| | || ||
Db        262 ATGGTCCATTCTCGACTGTCCTTACTCTCCGCTCGATTTCAACCCTCTCGACTTGGTCTG 321

Qy        228 GCTAGACACCACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGA 287
              ||| ||||| || || |||||||||||||||| |||||| ||||||| |||||| | ||
Db        322 GCTCGACACAACCAAACTTCTTTCTGCTGTCAATTGCTGGCTTAAGTGCATGGTGTTGGA 381

Qy        288 TCCTTATAATCAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGC 347
              ||||||  || || ||||| ||||| || || ||||| || || || ||||||||||| |
Db        382 TCCTTACAACCAGACAGATCATCCTGATTGCAAGTCCCGTCCGGATAGTGGTCTTTCTGG 441

Qy        348 CATCACAGAATTGGATCCAGGTTACATAACAGGTCCTCTTTC-TACTGTCTGGAAAGAGT 406
              ||| |||||| | |||||||||| |||||| | |||||||| | | || |||||||| |
Db        442 CATTACAGAACTTGATCCAGGTTATATAACAAGACCTCTTTCATTCAGTTTGGAAAGAAT 501

Qy        407 GGCTTAAGTGGTGTGTTGAGTTTGGTA 433
              || |||||||||| |||| ||||| |
Db        502 GGATTAAGTGGTGTATTGAATTTGGCA 528


RESULT 4
US-10-425-115-137717
; Sequence 137717, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137717
;   LENGTH: 924
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_57075C.1
US-10-425-115-137717

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  Matches  229;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy        239 CTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATC 298
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Db        590 CTCTGCTTTTCTCTGCGGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAATC 649

Qy        299 AAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAAT 358
              | | |||||||||||| || |||||| ||||||| |||||||||| || || |||||
Db        650 AGATAGACCATCCCGAATGCAAGTCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAGC 709

Qy        359 TGGATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGT 418
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Db        710 TGGACCCTGGTTATATAACAGGTCCTCTCTCTTCAGTATGGAAAGAATGGGTCAAATGGT 769

Qy        419 GTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGT 478
              |||| |||||||| || ||||| ||||||||| |||||||||| || |||||||| ||
Db        770 GTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCGTATGATTGGAGACTGC 829

Qy        479 CACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTT 527
              | ||| | |   | || ||| | || || |||||||||||  | |||||
Db        830 CCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAAATTAAAGTT 878


RESULT 5
US-10-425-115-93907
; Sequence 93907, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93907
;   LENGTH: 848
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_185630C.1
US-10-425-115-93907

  Query Match            11.4%;  Score 187.8;  DB 18;  Length 848;
  Best Local Similarity  77.3%;  Pred. No. 2.1e-47;
  Matches  228;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy        246 TCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAAACAGA 305
              | | ||||| || || |||||| |||| || ||| |||| || || |||||||| | |||
Db        387 TTTCTCTGCGGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAATCAGATAGA 446
```

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Qy        306 CCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCC 365
              ||||||||| || |||||| ||||||| |||||||||| || || |||||  |||| ||
Db        447 CCATCCCGAATGCAAGTCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAGCTGGACCC 506

Qy        366 AGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGTGTTGA 425
              |||||  |||||||||||||| ||| | || |||||||| ||| | || |||||||| ||
Db        507 TGGTTATATAACAGGTCCTCTCTCTTCAGTATGGAAAGAATGGGTCAAATGGTGTGTAGA 566

Qy        426 GTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCACCAAC 485
              ||||||  || |||||  |||||||| |||||||||| || |||||||| || | ||| |
Db        567 GTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCGTATGATTGGAGACTGCCCCCATC 626

Qy        486 CAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
              |    | || ||| | || || |||||||||||  | ||   || | | | | |
Db        627 AATGCTTGAGGAGAGAGATCTGTACTTTCACAAATTAAACAGGATCAGTAAGAGT 681


RESULT 6
US-10-425-115-93909
; Sequence 93909, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93909
;   LENGTH: 1383
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_185632C.1
US-10-425-115-93909

  Query Match             10.6%;  Score 173.8;  DB 18;  Length 1383;
  Best Local Similarity   76.8%;  Pred. No. 6.8e-43;
  Matches  228;  Conservative    0;  Mismatches   62;  Indels    7;  Gaps    1;

Qy        238 ACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAAT 297
              ||   |||| | ||| | || || |||||| |||| || ||| |||| || || ||||||
Db        696 ACATTGCTTTTCTCTACGGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAAT 755

Qy        298 CAAACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAA 357
              || |||||||||||||| || || ||| ||||||| |||||||||| || || |||||
Db        756 CAGACAGACCATCCCGAATGCAAATCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAG 815

Qy        358 TTGGATCCAGGTTACATAA-------CAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCT 410
              |||| || ||||| ||||       |||||||||| ||| | || |||||||| ||| |
Db        816 CTGGACCCTGGTTATATAACAGGTTTCAGGTCCTCTCTCTTCAGTATGGAAAGAATGGGT 875

Qy        411 TAAGTGGTGTGTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTG 470
              || |||||||| |||||||| || ||||| ||||||||| |||||||||| || |||||
Db        876 CAAATGGTGTGTAGAGTTTGGCATTGAAGCTAATGCAATTATCGCTGTTCCGTATGATTG 935

Qy        471 GAGATTGTCACCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTT 527
              |||| || | ||| | |   | || ||| | || || |||||||||||  | |||||
Db        936 GAGACTGCCCCCATCAATGCTTGAGGAGAGAGATCTGTACTTTCACAAATTAAAGTT 992


RESULT 7
US-10-424-599-17331
; Sequence 17331, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 17331
;   LENGTH: 1433
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(1433)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_115655C.1
US-10-424-599-17331

  Query Match             7.4%;  Score 120.8;  DB 16;  Length 1433;
  Best Local Similarity   70.5%;  Pred. No. 2.8e-26;
  Matches  186;  Conservative    0;  Mismatches   57;  Indels   21;  Gaps    1;

Qy        903 ATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATTAT 962
              ||| |||||||||||  |||| | | |  |||| |  ||||| ||||| ||||| || ||
Db         49 ATATCACTGTGATGAGCAGGAGTTTAAGACAAACTTATCTGGGTGGCCAACAAAAATAAT 108

Qy        963 TAACATTGAAATTCCTTCCACTAGCG--------------------TTACAGAAACAGC 1001
              |||||||||||||| || ||| | |                     |  |||||| | |
Db        109 CAACATTGAAATTCCCTCAACTCGTGCATTTGATGCATATCCTTCATTCTCAGAAATACC 168

Qy       1002 TCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCG 1061
              |   | |||| || |||||||||| || || || || || |  || |||||| |||| ||
Db        169 TGAGGCCAACTTGTCCAGCATGGAGTGCGGACTACCTACTCAATTATCTTTCTCAGCTCG 228

Qy       1062 TGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAG 1121
              ||| || ||||||| ||  ||||||| ||||| ||||| |||||||||||| ||||||||
Db        229 GGAAATATCAGATGGCACCTTTTTCAAGGCAATTGAAGATTATGACCCAGACAGCAAGAG 288

Qy       1122 GATGTTACACCAGTTAAAGAAGTT 1145
              | | ||  ||| |||| |||||||
Db        289 GCTCTTGTACCTGTTAGAGAAGTT 312


RESULT 8
US-10-424-599-57573
; Sequence 57573, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 57573
;   LENGTH: 380
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_22C.1
US-10-424-599-57573

  Query Match             4.4%;  Score 72.2;  DB 16;  Length 380;
  Best Local Similarity   61.2%;  Pred. No. 2e-11;
  Matches  167;  Conservative    0;  Mismatches  103;  Indels    3;  Gaps    3;

Qy       1234 AAGACAGAGGTTGGTTATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATC 1293
              ||   | |||  ||| | |||| ||| || ||  |  | || || |||||  | ||||||
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Db        109 AAAGAATAGGACGGTAACTACTATGCTCCTAGCCGTGAGCCCTACCCTGAACACTGGATC 168

Qy       1294 ATCACGGATATCAT-TTACGAAACTGAAGGTTCCCTCGTGTCAAGGTCTGGAACTGTGGT 1352
              || || | |  | | | |||| |  | ||| |  ||| ||   ||| |  | | |  |||
Db        169 ATTACTGTTGGCGTATCACGATAGCGCAGGATGTCTCTTGATCAGGACAAGGAATCCGGT 228

Qy       1353 TGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTACCCTATCATTCACTCTCTTG 1412
              ||  |||||| ||| | | ||| |  || |||||||||  || ||    || || |  ||
Db        229 TGGAGGGAACCCTGTATCCATAGC-CGGCATGAGACGGCGCCATACTTATCCCTTTTCTG 287

Qy       1413 GTGCAAGAATTGGCTCGGACCTAAAGTTAACATA-ACAATGGCTCCCCAGCCAGAACACG 1471
              | |||  ||  |||| || ||  | ||  ||||| |||   || || | |   || ||||
Db        288 GAGCAGAAACAGGCTTGGTCCGGATGTGCACATATACACAAGCCCCACCGTGTGAGCACG 347

Qy       1472 ATGGAAGCGACGTACATGTGGAACTAAATGTTG 1504
              | ||    || || ||  |  || |  |||| |
Db        348 AAGGGTCAGATGTTCACCTTAAATTGGATGTGG 380


RESULT 9
US-10-425-115-57116
; Sequence 57116, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 57116
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(369)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_152078C.1
US-10-425-115-57116

  Query Match             3.4%;  Score 56.6;  DB 18;  Length 369;
  Best Local Similarity   78.2%;  Pred. No. 1.5e-06;
  Matches   68;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy        238 ACTAAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAAT 297
              ||   |||| | ||||| || || |||||| |||| || ||| |||| || || ||||||
Db        283 ACATTGCTTTTCTCTGCAGTAAATTGCTGGCTTAAATGCATGCTGCTTGAACCCTATAAT 342

Qy        298 CAAACAGACCATCCCGAGTGTAAGTCA 324
              || | ||||||||||||| || ||||||
Db        343 CAGATAGACCATCCCGAATGCAAGTCA 369


RESULT 10
US-10-425-115-61794
; Sequence 61794, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 61794
;   LENGTH: 962
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_15634C.1
US-10-425-115-61794

  Query Match             3.1%;  Score 51;  DB 18;  Length 962;
  Best Local Similarity   80.0%;  Pred. No. 0.00016;
  Matches   60;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1555 GTTAAGTACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTC 1614
              || |||||||||||||  ||||| ||  |||| ||  |||| ||   |||||| ||||||
Db         32 GTGAAGTACATAACCTACTATGAGGATGCTGAAAGTCTTCCAGGATGGAGAACAGCAGTC 91

Qy       1615 TGGGAGCTTGATAAA 1629
              ||||||||  ||||||
Db         92 TGGGAGCTCGATAAA 106


RESULT 11
US-10-425-115-93908
; Sequence 93908, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 93908
;   LENGTH: 374
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_185631C.1
US-10-425-115-93908

  Query Match             2.7%;  Score 44;  DB 18;  Length 374;
  Best Local Similarity   83.3%;  Pred. No. 0.013;
  Matches   50;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy        321 GTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTGGATCCAGGTTACATAACAGG 380
              |||| ||||||| |||||||||| || || |||||  |||| || ||||| ||||||||
Db          1 GTCAAGGCCTGATAGTGGTCTTTCTGCAATTACAGAGCTGGACCCTGGTTATATAACAGG 60


RESULT 12
US-10-465-217-13/c
; Sequence 13, Application US/10465217
; Publication No. US20030204859A1
; GENERAL INFORMATION:
;  APPLICANT: Kazemi-Esfarjani, Parsa
;  APPLICANT:  Benzer, Seymour
;  TITLE OF INVENTION: AN ANIMAL MODEL OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY, METHODS OF USE, AND MODULATORS OF POLYGLUTAMINE
;  TITLE OF INVENTION:  TOXICITY
;  FILE REFERENCE: 06618-686001
;  CURRENT APPLICATION NUMBER: US/10/465,217
;  CURRENT FILING DATE:  2003-06-18
;  PRIOR APPLICATION NUMBER: US/09/639,207
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: US 60/148,934
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: US 60/148,933
;  PRIOR FILING DATE: 1999-08-12
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;  PRIOR APPLICATION NUMBER: US 60/177,047
;  PRIOR FILING DATE: 2000-01-18
;  PRIOR APPLICATION NUMBER: US 60/205,720
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 486
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic DNA
US-10-465-217-13

  Query Match             2.4%;  Score 38.8;  DB 15;  Length 486;
  Best Local Similarity   56.2%;  Pred. No. 0.67;
  Matches   73;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy        662 TTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAGG 721
              ||| |     | |   ||||  | | |||||||  ||| || || ||| | ||| ||  |
Db        183 TTGCTGCTGCTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTG 124

Qy        722 CAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCTC 781
              |  |      || || |   || ||   |  |||   || ||| | |||  |   |||||
Db        123 CTGTTGCTGCTGCTGTTGTTGCTGCTGCTGTTGCTGTTGCTGCTGCTGTTGCTGCTGCTG 64

Qy        782 GGTTGTTGTC 791
              ||  |||| |
Db         63 GGGGGTTGAC 54


RESULT 13
US-10-424-599-56537
; Sequence 56537, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56537
;   LENGTH: 1545
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_22062C.1
US-10-424-599-56537

  Query Match             2.3%;  Score 38;  DB 16;  Length 1545;
  Best Local Similarity   53.3%;  Pred. No. 2.5;
  Matches   80;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy        565 TCTATAGTATTTGCCCATTCAATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTG 624
              |||||  | || |  ||     ||| | |  || |||| | |   |      ||| ||||
Db        956 TCTATTTTTTTGGTGCAACAGTTGGTTTAGTATATCTTAATAACTTGGGACAAATAGCTG 1015

Qy        625 AGGCTAGAAATTGCACCAAAACATTATTTGAAGTGGCTTGATCAGCATATCCATGCTTAT 684
              |  | ||   |||| | || |  | ||| |   ||| |||  ||| |||       | || |
Db       1016 AATCCAGGGGTTGCTCTAATATTTCATCTTTGGTGTCTTTGTCATCATCGTTTGGGTTCT 1075

Qy        685 TTCGCTGTTGGAGCTCCTCTTCTTGGTTCT 714
              || || ||   |   | |||  |  || ||
Db       1076 TTGGCCGTCTCATGCCATCTCTTATGTACT 1105


RESULT 14
US-10-242-535A-23539
; Sequence 23539, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2005
;  CURRENT APPLICATION NUMBER: US/10/242,535A
;  CURRENT FILING DATE:  2002-09-12
;  PRIOR APPLICATION NUMBER: US 10/085,783
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: US 60/271,955
;  PRIOR FILING DATE: 2001-02-28
;  NUMBER OF SEQ ID NOS: 58994
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23539
;   LENGTH: 394
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (55)..(55)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (89)..(89)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (348)..(348)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (384)..(384)
;   OTHER INFORMATION: n is a, c, g, or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (389)..(389)
;   OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-23539

  Query Match             2.3%;  Score 37.6;  DB 16;  Length 394;
  Best Local Similarity   57.8%;  Pred. No. 1.4;
  Matches   67;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy        998 CAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAG 1057
              |||   |  | ||  | | || |    |   |||    |||| | || ||||||||  ||
Db        124 CAGGAGTTCTGAATGTCAGCATCTGCAAGAATGGTGCACCCATCATTATGTCTTTCCCAC 183

Qy       1058 CCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGAT 1113
              |  | | | |||||||| ||   || |    || |||||| |    ||||| ||
Db        184 ACTTTTACCAAGCAGATGAGAGGTTTGTTTCTGCCATAGAAGGCATGCACCCAAAT 239


RESULT 15
US-10-085-783A-23539
; Sequence 23539, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
;  APPLICANT: ChondroGene Inc.
;  APPLICANT:  Liew, C.C.
;  TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
;  FILE REFERENCE: 4231/2002
;  CURRENT APPLICATION NUMBER: US/10/085,783A
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/305,340
;  PRIOR FILING DATE: 2001-07-13
;  PRIOR APPLICATION NUMBER: US 60/275,017
;  PRIOR FILING DATE: 2001-03-12
```

; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23539
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55)..(55)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (89)..(89)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (348)..(348)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (384)..(384)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (389)..(389)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-23539

Query Match 2.3%; Score 37.6; DB 16; Length 394;
Best Local Similarity 57.8%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy        998 CAGCTCTAGTCAACATGACCAGCATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAG 1057
              |||   |  | ||  | | || |    |   |||    |||| | || |||||||| ||
Db        124 CAGGAGTTCTGAATGTCAGCATCTGCAAGAATGGTGCACCCATCATTATGTCTTTCCCAC 183

Qy       1058 CCCGTGAACTAGCAGATGGGACTCTTTTCAAAGCAATAGAAGACTATGACCCAGAT 1113
               |  | | | |||||||| ||   || |    || ||||||| |    ||||| ||
Db        184 ACTTTTACCAAGCAGATGAGAGGTTTGTTTCTGCCATAGAAGGCATGCACCCAAAT 239
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2004, 00:29:47 ; Search time 836 Seconds
(without alignments)
10304.187 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgaattcgaaatc.....ttgataaaagtgggtattaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	1641	100.0	1641	5	AAS01082	Aas01082 Arabidops
	2	1375	83.8	1902	12	ADF47823	Adf47823 Arabidops
	3	243	14.8	3896	3	AAC64438	Aac64438 Arabidops
	4	183	11.2	3896	3	AAC64448	Aac64448 Arabidops
	5	27	1.6	44	5	AAS01322	Aas01322 Arabidops
c	6	26	1.6	40	5	AAS01323	Aas01323 Arabidops
c	7	20	1.2	31140	4	AAL06791	Aal06791 Human rep
c	8	20	1.2	31140	4	ABA08065	Aba08065 Human ova
	9	20	1.2	226475	9	AAD58279	Aad58279 Human tum
c	10	19	1.2	407	3	AAA42733	Aaa42733 Human sec
c	11	19	1.2	453	4	ABA08624	Aba08624 Human sec
c	12	19	1.2	453	10	ADC32511	Adc32511 Human nov
c	13	19	1.2	909	3	AAC76568	Aac76568 Human ORF
c	14	19	1.2	1468	10	ADC30740	Adc30740 Human nov
c	15	19	1.2	1584	8	ACA21590	Aca21590 Prokaryot
c	16	19	1.2	2340	12	ADM72574	Adm72574 Nucleotid
c	17	19	1.2	2372	12	ADM72577	Adm72577 Nucleotid
c	18	19	1.2	2372	12	ADM72585	Adm72585 Nucleotid
c	19	19	1.2	2372	12	ADM72591	Adm72591 Nucleotid
c	20	19	1.2	2372	12	ADM72587	Adm72587 Nucleotid
c	21	19	1.2	2372	12	ADM72589	Adm72589 Nucleotid
c	22	19	1.2	2372	12	ADM72572	Adm72572 Nucleotid
c	23	19	1.2	2372	12	ADM72586	Adm72586 Nucleotid
c	24	19	1.2	2372	12	ADM72590	Adm72590 Nucleotid
c	25	19	1.2	2372	12	ADM72575	Adm72575 Nucleotid
c	26	19	1.2	2372	12	ADM72581	Adm72581 Nucleotid
c	27	19	1.2	2372	12	ADM72576	Adm72576 Nucleotid
c	28	19	1.2	2372	12	ADM72583	Adm72583 Nucleotid
c	29	19	1.2	2372	12	ADM72588	Adm72588 Nucleotid
c	30	19	1.2	2372	12	ADM72573	Adm72573 Nucleotid
c	31	19	1.2	2372	12	ADM72578	Adm72578 Nucleotid
c	32	19	1.2	2372	12	ADM72580	Adm72580 Nucleotid
c	33	19	1.2	2372	12	ADM72582	Adm72582 Nucleotid
c	34	19	1.2	2372	12	ADM72584	Adm72584 Nucleotid
c	35	19	1.2	2372	12	ADM72579	Adm72579 Nucleotid
c	36	19	1.2	2372	12	ADM72592	Adm72592 Nucleotid
	37	19	1.2	2488	2	AAV74418	Aav74418 Staphyloc
c	38	19	1.2	5331	4	AAK83053	Aak83053 Human imm
c	39	19	1.2	7022	4	AAK83051	Aak83051 Human imm
c	40	19	1.2	8495	10	ADC30133	Adc30133 Human nov
	41	19	1.2	13309	4	AAK83980	Aak83980 Human imm
c	42	19	1.2	172637	6	ABN83124	Abn83124 Human vol
c	43	19	1.2	237961	6	ABQ80552	Abq80552 Human Can
	44	18	1.1	125	3	AAC12300	Aac12300 Human sec
	45	18	1.1	153	3	AAC19008	Aac19008 Human sec
c	46	18	1.1	186	6	ABN90933	Abn90933 Staphyloc
	47	18	1.1	241	4	AAF17883	Aaf17883 Human bre
	48	18	1.1	241	4	AAS47313	Aas47313 Human bre
	49	18	1.1	241	6	ABS63914	Abs63914 Human bre
	50	18	1.1	241	10	ABT33126	Abt33126 Human tum
	51	18	1.1	241	11	ADL93033	Adl93033 Human bre
	52	18	1.1	241	12	ADE44323	Ade44323 Human cDN
	53	18	1.1	300	3	AAA00940	Aaa00940 Human col
c	54	18	1.1	309	10	ACF71748	Acf71748 Photorhab
	55	18	1.1	411	5	AAF66394	Aaf66394 Novel hum
	56	18	1.1	451	3	AAC66021	Aac66021 Human lun
	57	18	1.1	451	6	ABL49240	Abl49240 Human lun
	58	18	1.1	451	6	ABQ92426	Abq92426 Human lun
	59	18	1.1	451	9	ADA28415	Ada28415 Human lun
	60	18	1.1	451	10	ADH36979	Adh36979 Human lun
	61	18	1.1	451	12	ADM56782	Adm56782 Human lun
	62	18	1.1	458	4	AAH55550	Aah55550 Human bre
	63	18	1.1	458	12	ADN40320	Adn40320 Human bre
	64	18	1.1	489	3	AAC23414	Aac23414 Human sec
c	65	18	1.1	516	6	ABK44558	Abk44558 cDNA enco
c	66	18	1.1	545	6	ABV87927	Abv87927 Human col
	67	18	1.1	578	5	ABV53961	Abv53961 Human pro
c	68	18	1.1	738	10	ACF68308	Acf68308 Photorhab
c	69	18	1.1	784	5	AAS82779	Aas82779 DNA encod
	70	18	1.1	792	6	ABZ13450	Abz13450 Arabidops
	71	18	1.1	792	6	ADG88173	Adg88173 A. thalia
	72	18	1.1	792	8	ADA68169	Ada68169 Arabidops
	73	18	1.1	889	3	AAC33097	Aac33097 Arabidops
c	74	18	1.1	912	2	AAT03477	Aat03477 Transcrip
	75	18	1.1	912	3	AAC32847	Aac32847 Arabidops
	76	18	1.1	920	3	AAC50553	Aac50553 Arabidops
c	77	18	1.1	1024	6	ABX66911	Abx66911 Helicobac
c	78	18	1.1	1232	4	AAI58782	Aai58782 Human pol
c	79	18	1.1	1232	5	ADQ99002	Adq99002 DNA encod
c	80	18	1.1	1232	9	ADB48762	Adb48762 Novel hum
c	81	18	1.1	1422	8	ABZ77721	Abz77721 Nucleotid
c	82	18	1.1	1539	4	AAF71124	Aaf71124 C. glutam
c	83	18	1.1	1543	2	AAX14307	Aax14307 H. pylori
c	84	18	1.1	1554	5	AAH66546	Aah66546 C glutami
c	85	18	1.1	1603	9	ACC59460	Acc59460 C glutami
	86	18	1.1	1653	3	AAC41704	Aac41704 Arabidops
	87	18	1.1	1747	2	AAZ24893	Aaz24893 Human sec
	88	18	1.1	1747	8	ADA40096	Ada40096 Human sec
	89	18	1.1	1747	8	ACC50600	Acc50600 Human sec
	90	18	1.1	1747	10	ADC73671	Adc73671 Human sec
	91	18	1.1	1747	10	ADA56270	Ada56270 Gene enco
	92	18	1.1	1748	10	ADB58615	Adb58615 Toxicity-
	93	18	1.1	1748	10	ADB53263	Adb53263 Primary r
c	94	18	1.1	1947	2	AAX61429	Aax61429 DNA encod

	95	18	1.1	2209	4	AAH19237 Aah19237 Human sec
	96	18	1.1	2304	6	ABZ66863 Abz66863 Arabidops
	97	18	1.1	2352	3	AAC51596 Aac51596 Arabidops
c	98	18	1.1	2414	4	AAH14270 Aah14270 Human cDN
c	99	18	1.1	2414	8	ACC50994 Acc50994 Human bla
c	100	18	1.1	2414	12	ADN04937 Adn04937 Antipsori
c	101	18	1.1	2459	4	AAI60568 Aai60568 Human pol
	102	18	1.1	2509	4	AAF62693 Aaf62693 Arabidops
	103	18	1.1	2548	5	AAS82714 Aas82714 DNA encod
c	104	18	1.1	2701	2	AAX86143 Aax86143 DNA encod
	105	18	1.1	3238	4	AAK52242 Aak52242 Human pol
	106	18	1.1	3268	10	ADF76738 Adf76738 Novel hum
c	107	18	1.1	3278	2	AAT62358 Kluyverom
c	108	18	1.1	3278	2	AAT73285 Aat73285 K. lactis
	109	18	1.1	3459	8	ABZ33708 Abz33708 Human col
	110	18	1.1	3521	3	AAZ57791 Aaz57791 5' upstre
	111	18	1.1	3582	8	ACF39318 Acf39318 Mycobacte
c	112	18	1.1	3887	4	AAH14236 Aah14236 Human cDN
c	113	18	1.1	3887	12	ADQ18922 Adq18922 Human sof
c	114	18	1.1	4027	6	ABQ99318 Abq99318 Human cod
	115	18	1.1	4382	9	ABQ80410 Abq80410 AAV9 rep
	116	18	1.1	4385	10	ADE76506 Ade76506 Adeno-ass
c	117	18	1.1	4470	10	ADH28791 Adh28791 Human chr
c	118	18	1.1	4470	12	ADP13530 Adp13530 Renal cel
	119	18	1.1	4509	4	AAI60167 Aai60167 Human pol
	120	18	1.1	4586	4	AAI58642 Aai58642 Human pol
	121	18	1.1	4586	5	ADQ98860 Adq98860 DNA encod
	122	18	1.1	4586	9	ADB48620 Adb48620 Novel hum
	123	18	1.1	4684	3	AAA62904 Aaa62904 Murine JN
	124	18	1.1	4820	4	AAI60428 Aai60428 Human pol
c	125	18	1.1	5425	5	AAS82780 Aas82780 DNA encod
c	126	18	1.1	5473	4	AAI58381 Aai58381 Human pol
c	127	18	1.1	5473	5	ADQ98590 Adq98590 DNA encod
c	128	18	1.1	5473	9	ADB48350 Adb48350 Novel hum
	129	18	1.1	5581	10	ADE54007 Ade54007 Human pro
c	130	18	1.1	6412	4	ABL19284 Abl19284 Drosophil
c	131	18	1.1	6450	10	ABZ23178 Abz23178 Polynucle
c	132	18	1.1	6450	12	ADN36880 Adn36880 P200 nucl
c	133	18	1.1	6539	10	ADE57349 Ade57349 Human gen
c	134	18	1.1	7545	8	AAL50282 Aal50282 Human nuc
	135	18	1.1	10166	8	ABX76359 Abx76359 Lung canc
	136	18	1.1	10166	8	ACD13432 Acd13432 Human DNA
	137	18	1.1	10166	11	ADN38843 Adn38843 Cancer/an
	138	18	1.1	10172	6	ABL65392 Abl65392 Lung canc
	139	18	1.1	10172	12	ADQ18203 Adq18203 Human sof
	140	18	1.1	10175	5	AAS70589 Aas70589 DNA encod
	141	18	1.1	10284	8	ABX77543 Abx77543 Different
	142	18	1.1	10284	8	ABX63047 Abx63047 Human cDN
	143	18	1.1	10411	12	ADQ22757 Adq22757 Human sof
c	144	18	1.1	10853	12	ADQ23295 Adq23295 Human sof
	145	18	1.1	44576	11	ADL27116 Adl27116 Human gen
	146	18	1.1	44577	9	ADA03038 Ada03038 Human ROR
	147	18	1.1	44577	9	ADA66322 Ada66322 Human ROR
	148	18	1.1	44577	10	ADB72776 Adb72776 Human ROR
	149	18	1.1	110000	4	AAI99682_02 Continuation (3 of
	150	18	1.1	110000	4	AAI99683_02 Continuation (3 of
c	151	18	1.1	110000	6	ABS55320_1 Continuation (2 of
c	152	18	1.1	110000	10	ACF67367_10 Continuation (11 o
c	153	18	1.1	110000	10	ACF67367_49 Continuation (50 o
c	154	18	1.1	110000	10	ACF65387_0 Acf65387 Photorhab
c	155	18	1.1	110000	10	ACF65384_4 Continuation (5 of
	156	18	1.1	151826	3	AAF22291 Aaf22291 BAC conta
c	157	18	1.1	341511	6	ABS55200 Abs55200 Genomic D
c	158	18	1.1	349980	5	AAH68529 Aah68529 C glutami
c	159	18	1.1	349980	5	AAH68528 Aah68528 C glutami
c	160	17	1.0	24	8	ABV76847 Abv76847 Probe for
	161	17	1.0	25	9	ACI26248 Aci26248 Human mic
	162	17	1.0	25	9	ACI46356 Aci46356 Human mic
c	163	17	1.0	47	10	ADC87714 Adc87714 Primer fo
c	164	17	1.0	60	6	ABN38582 Abn38582 Human spl
	165	17	1.0	76	12	ACH84147 Ach84147 Human gen
c	166	17	1.0	149	3	AAC18153 Aac18153 Human sec
	167	17	1.0	191	3	AAC30031 Aac30031 Human sec
c	168	17	1.0	200	10	ADC71569 Adc71569 SPC6-spec
c	169	17	1.0	201	2	AAH85669 Aah85669 Human sin
	170	17	1.0	237	4	AAS53779 Aas53779 Helicobac
	171	17	1.0	254	6	ABL38186 Abl38186 Human col
c	172	17	1.0	274	10	ABX87779 Abx87779 Corn ear-
	173	17	1.0	278	5	ADL40011 Adl40011 Human ova
	174	17	1.0	296	2	AAZ13059 Aaz13059 Human gen
	175	17	1.0	300	2	AAZ14785 Aaz14785 Human gen
c	176	17	1.0	303	10	ADC75311 Adc75311 T harzian
c	177	17	1.0	321	10	ADH83348 Adh83348 Enterococ
c	178	17	1.0	372	3	AAC74612 Aac74612 Human ORF
c	179	17	1.0	372	6	ABN25879 Abn25879 Human ORF
c	180	17	1.0	387	5	ADI68348 Adi68348 Human ova
c	181	17	1.0	387	5	ADI74714 Adi74714 Human ova
	182	17	1.0	387	8	ABX46449 Abx46449 Bovine ES
	183	17	1.0	404	6	ABL62985 Abl62985 Breast ca
	184	17	1.0	404	6	ABL62801 Abl62801 Breast ca
c	185	17	1.0	424	6	ABN19298 Abn19298 Human ORF
	186	17	1.0	426	8	ABZ18618 Abz18618 Group III
c	187	17	1.0	438	5	ADL39951 Adl39951 Human ova
c	188	17	1.0	444	4	AAI85462 Aai85462 Human pol
c	189	17	1.0	454	4	AAK65366 Aak65366 Human imm
	190	17	1.0	473	5	ABA19054 Aba19054 Human ner
c	191	17	1.0	487	9	ACH19034 Ach19034 Human adu
	192	17	1.0	504	12	ACH70447 Ach70447 Human gen
	193	17	1.0	520	6	ABQ20867 Abq20867 Oligonucl
c	194	17	1.0	520	6	ABQ20866 Abq20866 Oligonucl
c	195	17	1.0	527	6	ABQ19486 Abq19486 Oligonucl
	196	17	1.0	527	6	ABQ19487 Abq19487 Oligonucl
	197	17	1.0	534	4	AAH12238 Aah12238 Human cDN
c	198	17	1.0	534	8	ABX98493 Abx98493 Rice albu
	199	17	1.0	541	4	AAH10604 Aah10604 Human cDN
c	200	17	1.0	547	4	ABA61179 Aba61179 Human foe
c	201	17	1.0	547	4	AAI41079 Aai41079 Probe #97
c	202	17	1.0	547	4	AAK35366 Aak35366 Human bon
c	203	17	1.0	547	4	AAK09474 Aak09474 Human bra
c	204	17	1.0	547	4	ABS35104 Abs35104 Human liv
c	205	17	1.0	551	8	ABZ51545 Abz51545 Aspergill
c	206	17	1.0	574	5	ADL45825 Adl45825 Human ova
	207	17	1.0	575	4	AAH10044 Aah10044 Human cDN
c	208	17	1.0	576	6	ABV88921 Abv88921 Human col
	209	17	1.0	585	6	ABQ49033 Abq49033 Oligonucl
c	210	17	1.0	585	6	ABQ49032 Abq49032 Oligonucl
c	211	17	1.0	591	10	ADG76925 Adg76925 Hepatitis
c	212	17	1.0	593	6	ABK35823 Abk35823 cDNA sequ
c	213	17	1.0	663	6	ABL92616 Abl92616 Chlamydia
c	214	17	1.0	666	10	ADD43915 Add43915 Chlamydia
	215	17	1.0	709	2	AAZ15236 Aaz15236 Human gen
c	216	17	1.0	715	6	ABQ38216 Abq38216 Oligonucl
	217	17	1.0	715	6	ABQ38217 Abq38217 Oligonucl
c	218	17	1.0	719	2	AAT78167 Aat78167 Human den
c	219	17	1.0	723	4	AAI95333 Aai95333 Human neu
c	220	17	1.0	750	10	ADC78912 Adc78912 Human PRO
c	221	17	1.0	754	10	ACA55445 Aca55445 Human sig
c	222	17	1.0	754	12	ADI55241 Adi55241 Human pol
c	223	17	1.0	760	6	ABL62626 Abl62626 Colon ade
c	224	17	1.0	760	6	ABL68646 Abl68646 Kidney ca
c	225	17	1.0	793	3	AAF18330 Aaf18330 Lung canc
c	226	17	1.0	803	6	ABT07742 Abt07742 Breast ca
c	227	17	1.0	803	11	ADN39646 Adn39646 Cancer/an
c	228	17	1.0	803	12	ADN04461 Adn04461 Antipsori
	229	17	1.0	807	10	ABX78322 Abx78322 Soybean s
	230	17	1.0	810	4	ABL16017 Abl16017 Drosophil
	231	17	1.0	810	5	ABA20661 Aba20661 Human ner
c	232	17	1.0	810	8	ACA19270 Aca19270 Prokaryot
	233	17	1.0	819	6	ABN98968 Abn98968 Arabidops
	234	17	1.0	828	2	AAZ16375 Aaz16375 Human gen
	235	17	1.0	846	2	AAX37420 Aax37420 Human sec
	236	17	1.0	896	5	ABA20660 Aba20660 Human ner
c	237	17	1.0	906	11	ABD17107 Abd17107 Pseudomon
	238	17	1.0	966	9	ADA32214 Ada32214 DNA encod
c	239	17	1.0	978	5	AAS68024 Aas68024 DNA encod
	240	17	1.0	980	12	ADJ44103 Adj44103 Plant cDN

	241	17	1.0	983	4	AAL23433 Aal23433 Human bre
c	242	17	1.0	1007	11	ADL80120 Adl80120 Rat GLAR2
c	243	17	1.0	1011	3	AAC76341 Aac76341 Human ORF
	244	17	1.0	1026	10	ABX78323 Abx78323 Soybean s
	245	17	1.0	1044	3	AAC44684 Aac44684 Arabidops
	246	17	1.0	1083	6	ABZ14418 Abz14418 Arabidops
	247	17	1.0	1083	8	ADA68162 Ada68162 Arabidops
c	248	17	1.0	1093	4	AAS63235 Aas63235 Escherich
	249	17	1.0	1095	11	ACH95859 Ach95859 Klebsiell
c	250	17	1.0	1122	9	ADA31773 Ada31773 DNA encod
c	251	17	1.0	1174	12	ADQ24977 Adq24977 Human sof
	252	17	1.0	1209	6	ABN67412 Abn67412 Streptoco
	253	17	1.0	1209	6	ABN69169 Abn69169 Streptoco
	254	17	1.0	1251	10	ADC93361 Adc93361 E. faeciu
	255	17	1.0	1314	3	AAC33762 Aac33762 Arabidops
	256	17	1.0	1341	12	ADM16727 Adm16727 PERL-P7-G
c	257	17	1.0	1388	6	ABL65839 Abl65839 Lung canc
c	258	17	1.0	1388	6	ABL66504 Abl66504 Lung canc
c	259	17	1.0	1389	10	ADA19248 Ada19248 Human ins
c	260	17	1.0	1389	12	ADL72157 Adl72157 Human sol
c	261	17	1.0	1389	12	ADL71958 Adl71958 Human CEN
c	262	17	1.0	1389	12	ADP07277 Adp07277 Human CEN
c	263	17	1.0	1389	12	ADQ18940 Adq18940 Human sof
	264	17	1.0	1434	3	AAA57987 Aaa57987 1434 bp C
	265	17	1.0	1438	3	AAA57944 Aaa57944 1438 bp C
	266	17	1.0	1483	4	ABL13137 Abl13137 Drosophil
c	267	17	1.0	1542	4	ABL29073 Abl29073 Drosophil
c	268	17	1.0	1548	11	ABD17076 Abd17076 Pseudomon
c	269	17	1.0	1551	10	ACC60634 Acc60634 Gene sequ
c	270	17	1.0	1551	10	ADK62575 Adk62575 Disease t
c	271	17	1.0	1554	5	AAS77325 Aas77325 DNA encod
	272	17	1.0	1587	3	AAC45864 Aac45864 Arabidops
	273	17	1.0	1591	3	AAC40192 Aac40192 Arabidops
	274	17	1.0	1626	9	ADB12548 Adb12548 Alloiococ
	275	17	1.0	1626	9	ADB12546 Adb12546 Alloiococ
c	276	17	1.0	1647	10	ACF70647 Acf70647 Photorhab
c	277	17	1.0	1750	3	AAZ86992 Aaz86992 Retinobla
c	278	17	1.0	1803	12	ADQ23308 Adq23308 Human sof
	279	17	1.0	1806	10	ADC32551 Adc32551 Human nov
	280	17	1.0	1871	6	ABL49882 Abl49882 Human euk
	281	17	1.0	1936	4	ABL18501 Abl18501 Drosophil
	282	17	1.0	1936	10	ADK11422 Adk11422 Drosophil
c	283	17	1.0	1980	4	ABL24095 Abl24095 Drosophil
c	284	17	1.0	2000	6	ABZ16197 Abz16197 Arabidops
	285	17	1.0	2000	6	ABZ16817 Abz16817 Arabidops
c	286	17	1.0	2000	8	ADA72020 Ada72020 Rice gene
c	287	17	1.0	2000	10	ACC61539 Acc61539 Gene sequ
c	288	17	1.0	2000	10	ADK64487 Adk64487 Disease t
c	289	17	1.0	2005	4	AAH15825 Aah15825 Human cDN
c	290	17	1.0	2005	5	AAI93872 Aai93872 Human sto
c	291	17	1.0	2006	4	AAS31191 Aas31191 Human dia
c	292	17	1.0	2018	4	AAS36068 Aas36068 Human car
c	293	17	1.0	2018	10	ADE46762 Ade46762 Human car
	294	17	1.0	2021	10	ADC30797 Adc30797 Human nov
c	295	17	1.0	2046	4	ABL18077 Abl18077 Drosophil
	296	17	1.0	2063	10	ADB62301 Adb62301 Human cDN
c	297	17	1.0	2200	9	ADA09943 Ada09943 Plasmid K
c	298	17	1.0	2200	11	ADL80088 Adl80088 Rat galan
c	299	17	1.0	2200	12	ADG41992 Adg41992 Rat Galac
	300	17	1.0	2235	8	ACA53680 Aca53680 Prokaryot
	301	17	1.0	2237	4	ABL13285 Abl13285 Drosophil
	302	17	1.0	2260	8	ABZ21288 Abz21288 Soybean n
c	303	17	1.0	2262	8	ABX34683 Abx34683 Human mdd
c	304	17	1.0	2271	4	AAH17984 Aah17984 Human cDN
	305	17	1.0	2273	3	AAZ52462 Aaz52462 HTRM clon
c	306	17	1.0	2300	2	AAT62735 Aat62735 Herbicide
	307	17	1.0	2310	8	ACA30150 Aca30150 Prokaryot
	308	17	1.0	2346	12	ADQ18626 Adq18626 Human sof
	309	17	1.0	2347	12	ADG32215 Adg32215 DNA encod
	310	17	1.0	2385	3	AAC83331 Aac83331 PART-1 pr
c	311	17	1.0	2520	10	ADA52554 Ada52554 Human cod
	312	17	1.0	2548	12	ADI27256 Adi27256 Human cDN
	313	17	1.0	2601	8	ACA36853 Aca36853 Prokaryot
	314	17	1.0	2634	4	ABL23066 Abl23066 Drosophil
c	315	17	1.0	2666	4	AAI61029 Aai61029 Human pol
	316	17	1.0	2674	5	ADL46031 Adl46031 Human ova
	317	17	1.0	2706	4	AAH17855 Aah17855 Human cDN
	318	17	1.0	2747	4	ABL13132 Abl13132 Drosophil
	319	17	1.0	2781	11	ADM02100 Adm02100 Human cDN
c	320	17	1.0	2799	4	AAS31406 Aas31406 Human cDN
c	321	17	1.0	2799	6	ABQ66730 Abq66730 Human pol
c	322	17	1.0	2799	10	ADC10752 Adc10752 Human cDN
	323	17	1.0	2822	11	ADM02578 Adm02578 Human cDN
	324	17	1.0	2834	10	ADF38007 Adf38007 Synchroni
c	325	17	1.0	2931	4	AAH14627 Aah14627 Human cDN
c	326	17	1.0	2975	6	ABQ69192 Abq69192 Listeria
	327	17	1.0	2996	4	AAH16299 Aah16299 Human cDN
	328	17	1.0	2996	12	ADN04821 Adn04821 Antipsori
	329	17	1.0	3044	4	AAS31284 Aas31284 Human cDN
	330	17	1.0	3044	6	ABQ66608 Abq66608 Human pol
	331	17	1.0	3044	10	ADC10630 Adc10630 Human cDN
c	332	17	1.0	3081	4	AAH16266 Aah16266 Human cDN
c	333	17	1.0	3126	2	AAQ42425 Aaq42425 ADA3 DNA.
c	334	17	1.0	3132	11	ADM01994 Adm01994 Human cDN
c	335	17	1.0	3145	9	ACH04114 Ach04114 Human cDN
c	336	17	1.0	3246	5	ABV25849 Abv25849 Human pro
c	337	17	1.0	3247	5	ABV24853 Abv24853 Human pro
c	338	17	1.0	3406	4	ABL03126 Abl03126 Drosophil
c	339	17	1.0	3469	4	ABL16016 Abl16016 Drosophil
	340	17	1.0	3536	4	ABL13136 Abl13136 Drosophil
	341	17	1.0	3655	11	ADP09778 Adp09778 Complete
	342	17	1.0	3715	10	ADA53498 Ada53498 Human cod
	343	17	1.0	3805	4	ABL07900 Abl07900 Drosophil
c	344	17	1.0	3846	4	ABA08642 Aba08642 Human ret
	345	17	1.0	3980	4	ABL24094 Abl24094 Drosophil
c	346	17	1.0	4063	4	ABL18500 Abl18500 Drosophil
c	347	17	1.0	4071	6	ABQ70833 Abq70833 Listeria
	348	17	1.0	4140	8	ACD13197 Acd13197 cDNA enco
c	349	17	1.0	4149	6	ABK97892 Abk97892 DNA encod
c	350	17	1.0	4226	4	AAI58593 Aai58593 Human pol
c	351	17	1.0	4226	5	ADQ98810 Adq98810 DNA encod
c	352	17	1.0	4226	9	ADB48570 Adb48570 Novel hum
c	353	17	1.0	4238	4	ABL18076 Abl18076 Drosophil
	354	17	1.0	4264	4	AAI60379 Aai60379 Human pol
	355	17	1.0	4400	4	ABL29072 Abl29072 Drosophil
c	356	17	1.0	4521	4	AAI59243 Aai59243 Human pol
c	357	17	1.0	4674	5	ABA83068 Aba83068 Human tra
	358	17	1.0	4933	10	ADF78188 Adf78188 Human ext
c	359	17	1.0	5298	3	AAC76822 Aac76822 Human ORF
	360	17	1.0	5411	10	ADB85523 Adb85523 Human GIG
	361	17	1.0	5411	10	ADC16738 Adc16738 Human mod
	362	17	1.0	5474	2	AAQ90251 Aaq90251 Tuberous
	363	17	1.0	5525	12	ADQ22998 Adq22998 Human sof
	364	17	1.0	5526	5	AAS76845 Aas76845 DNA encod
	365	17	1.0	5543	10	ADB85524 Adb85524 Human GIG
	366	17	1.0	5543	10	ADC16739 Adc16739 Human mod
	367	17	1.0	5543	12	ADQ18516 Adq18516 Human sof
	368	17	1.0	5546	10	ADG42120 Adg42120 Human bra
c	369	17	1.0	5659	8	ABX62964 Abx62964 Human act
	370	17	1.0	5760	4	ABL17696 Abl17696 Drosophil
c	371	17	1.0	5763	8	ABX62963 Abx62963 Human act
	372	17	1.0	5778	4	AAK53086 Aak53086 Human pol
	373	17	1.0	5804	4	AAK52102 Aak52102 Human pol
c	374	17	1.0	6002	3	AAZ86968 Aaz86968 Retinobla
	375	17	1.0	6291	4	ABL06646 Abl06646 Drosophil
c	376	17	1.0	6810	10	ADE07807 Ade07807 Novel cod
c	377	17	1.0	6946	4	ABL26952 Abl26952 Drosophil
c	378	17	1.0	7459	6	ABK31382 Abk31382 Signal tr
	379	17	1.0	7786	6	ABA92788 Aba92788 Buchnera
c	380	17	1.0	8733	4	ABL29304 Abl29304 Drosophil
	381	17	1.0	11169	6	ABQ67095 Abq67095 Human ang
	382	17	1.0	11622	6	ABL32675 Abl32675 Human imm
c	383	17	1.0	12595	4	AAS42100 Aas42100 Genomic s
c	384	17	1.0	13236	12	ADQ21058 Adq21058 Human sof
c	385	17	1.0	13788	5	ABA19999 Aba19999 Human ner
	386	17	1.0	13855	10	ADE79055 Ade79055 Human pro

c 387	17	1.0	15009	4	ABL13813	Abl13813 Drosophil
c 388	17	1.0	15330	5	ABA15821	Aba15821 Human ner
c 389	17	1.0	15463	4	AAK86350	Aak86350 Human imm
c 390	17	1.0	18028	4	ABL13284	Abl13284 Drosophil
c 391	17	1.0	19034	4	ABL13812	Abl13812 Drosophil
c 392	17	1.0	19734	6	ABL33932	Abl33932 Human imm
c 393	17	1.0	19798	10	ADD71026	Add71026 Human nth
c 394	17	1.0	22744	9	ADA02915	Ada02915 Mouse Fus
c 395	17	1.0	22744	10	ADB72653	Adb72653 Mouse Fus
c 396	17	1.0	22744	10	ADC85395	Adc85395 Mouse Fus
c 397	17	1.0	22744	12	ADM74510	Adm74510 Murine ca
c 398	17	1.0	24800	9	ADA02921	Ada02921 Mouse Ras
c 399	17	1.0	24800	10	ADB72659	Adb72659 Mouse Ras
c 400	17	1.0	24800	10	ADC85401	Adc85401 Mouse Ras
c 401	17	1.0	24800	12	ADM74516	Adm74516 Murine ca
c 402	17	1.0	25231	4	AAL03112	Aal03112 Human rep
c 403	17	1.0	26201	6	ABK14446	Abk14446 Human HMG
c 404	17	1.0	26201	6	ABK14039	Abk14039 Human 3-h
c 405	17	1.0	28001	12	ADI36729	Adi36729 Genomic D
c 406	17	1.0	28001	12	ADI36730	Adi36730 Genomic D
c 407	17	1.0	28001	12	ADM93169	Adm93169 Human KOX
c 408	17	1.0	28001	12	ADM93170	Adm93170 Human KOX
c 409	17	1.0	29521	4	AAS32517	Aas32517 Human gen
c 410	17	1.0	29543	4	AAS32516	Aas32516 Human gen
c 411	17	1.0	30393	4	AAK67239	Aak67239 Human imm
c 412	17	1.0	32038	4	AAK90877	Aak90877 Human dig
c 413	17	1.0	32038	4	AAK89980	Aak89980 Human dig
c 414	17	1.0	32038	5	AAS30028	Aas30028 Human lun
c 415	17	1.0	32038	10	ADB33365	Adb33365 Human nov
416	17	1.0	32844	12	ADJ12644	Adj12644 DNA fragm
c 417	17	1.0	35100	2	AAV73802	Aav73802 KSHV LUR
418	17	1.0	44147	6	ABK84481	Abk84481 Human cDN
419	17	1.0	44147	10	ADD14691	Add14691 Human src
420	17	1.0	50335	9	AAD58280	Aad58280 Human tum
421	17	1.0	50885	4	AAK70336	Aak70336 Human imm
422	17	1.0	52302	9	ADA02738	Ada02738 Human CCN
423	17	1.0	52302	10	ADB72476	Adb72476 Human CCN
424	17	1.0	52302	10	ADC85218	Adc85218 Human Ccn
425	17	1.0	52302	12	ADM74333	Adm74333 Human car
426	17	1.0	54297	4	AAK70625	Aak70625 Human imm
427	17	1.0	55001	12	ADG88848	Adg88848 Human Not
428	17	1.0	55001	12	ADH74825	Adh74825 Human Not
c 429	17	1.0	63155	10	ADC85996	Adc85996 Human GPC
c 430	17	1.0	65359	6	AAD46665	Aad46665 Human tra
c 431	17	1.0	86000	12	ADP68568	Adp68568 Human PPA
c 432	17	1.0	96597	9	ADA02597	Ada02597 Mouse Run
c 433	17	1.0	96597	10	ADB72335	Adb72335 Mouse Run
c 434	17	1.0	96597	10	ADE95845	Ade95845 Mouse Run
435	17	1.0	97658	8	ABQ83210_3	Continuation (4 of
c 436	17	1.0	106344	10	ADJ79961	Adj79961 Full leng
c 437	17	1.0	110000	2	AAV21209_10	Continuation (11 o
438	17	1.0	110000	2	AAZ01425_06	Continuation (7 of
c 439	17	1.0	110000	4	AAK95240_01	Continuation (2 of
440	17	1.0	110000	4	AAI99682_00	Aai99682 Mycobacte
441	17	1.0	110000	4	AAI99683_00	Aai99683 Mycobacte
c 442	17	1.0	110000	4	AAK96733_01	Continuation (2 of
c 443	17	1.0	110000	6	ABN71527_11	Continuation (12 o
c 444	17	1.0	110000	6	ABN71527_20	Continuation (21 o
c 445	17	1.0	110000	6	ABT00010_01	Continuation (2 of
c 446	17	1.0	110000	6	ABX08336_01	Continuation (2 of
c 447	17	1.0	110000	6	ABQ69245_10	Continuation (11 o
c 448	17	1.0	110000	6	ABQ67197_09	Continuation (10 o
c 449	17	1.0	110000	6	ABT01503_01	Continuation (2 of
c 450	17	1.0	110000	6	ABA03041_10	Continuation (11 o
451	17	1.0	110000	6	ABA03041_16	Continuation (17 o
c 452	17	1.0	110000	8	ABQ83210_1	Continuation (2 of
c 453	17	1.0	110000	8	AAD53223_1	Continuation (2 of
c 454	17	1.0	110000	9	ADB12064_16	Continuation (17 o
455	17	1.0	110000	10	ADF77343_09	Continuation (10 o
c 456	17	1.0	110000	10	ACF67367_37	Continuation (38 o
457	17	1.0	110000	10	ACF65388_10	Continuation (11 o
458	17	1.0	110000	11	ADM27081_14	Continuation (15 o
459	17	1.0	110000	11	ADM27081_15	Continuation (16 o
c 460	17	1.0	110000	12	ADH77486_01	Continuation (2 of
c 461	17	1.0	110000	12	ADJ25985_01	Continuation (2 of
c 462	17	1.0	110000	12	ADN97989_01	Continuation (2 of
c 463	17	1.0	110000	12	ADO50281_01	Continuation (2 of
464	17	1.0	112604	12	ADQ18153	Adq18153 Human sof
465	17	1.0	127098	10	ADL13649	Adl13649 Osteoarth
466	17	1.0	134525	2	AAQ04525	Aaq04525 Total bas
c 467	17	1.0	137507	2	AAV19941	Aav19941 KSHV long
c 468	17	1.0	137508	12	ADN12162	Adn12162 Human her
c 469	17	1.0	139032	6	ABQ79105	Abq79105 Human for
c 470	17	1.0	139257	10	ADC89520	Adc89520 Human COR
471	17	1.0	158091	12	ADL08119	Adl08119 Human gen
c 472	17	1.0	162450	3	AAZ86967	Aaz86967 Retinobla
473	17	1.0	174566	8	ABQ77400	Abq77400 Human ITG
474	17	1.0	174566	12	ADL08118	Adl08118 Human gen
475	17	1.0	185035	6	ABT10147	Abt10147 Human bre
476	17	1.0	185035	8	ACA64951	Aca64951 Human FEN
477	17	1.0	185035	12	ADQ20284	Adq20284 Human sof
478	17	1.0	197997	10	AAL54074	Aal54074 Human tra
479	17	1.0	216215	10	ADF69167	Adf69167 Human MP5
c 480	17	1.0	236303	4	AAS11614	Aas11614 Human gen
481	17	1.0	335913	5	AAI61371	Aai61371 Soybean 2
482	17	1.0	335913	5	AAI61372	Aai61372 Soybean 2
483	16	1.0	24	12	ADP20304	Adp20304 Human GPC
484	16	1.0	25	9	ACI64906	Aci64906 Human mic
485	16	1.0	25	9	ACK11391	Ack11391 Human mic
486	16	1.0	41	6	ABZ43786	Abz43786 Human N-a
487	16	1.0	41	6	ABZ50823	Abz50823 Human N-a
488	16	1.0	60	6	ABN32576	Abn32576 Human spl
489	16	1.0	65	6	ABN28763	Abn28763 Rat splic
c 490	16	1.0	88	12	ACH81606	Ach81606 Human gen
491	16	1.0	112	4	AAL07391	Aal07391 Human rep
492	16	1.0	112	4	AAL07392	Aal07392 Human rep
493	16	1.0	112	4	ABA08195	Aba08195 Human ova
494	16	1.0	112	4	ABA08194	Aba08194 Human ova
495	16	1.0	116	4	AAK17867	Aak17867 Human bra
496	16	1.0	116	4	ABS43394	Abs43394 Human liv
c 497	16	1.0	129	4	ABA71834	Aba71834 Human foe
c 498	16	1.0	129	4	AAI52178	Aai52178 Probe #20
c 499	16	1.0	129	4	AAK46279	Aak46279 Human bon
c 500	16	1.0	129	4	AAK20210	Aak20210 Human bra
c 501	16	1.0	129	4	ABS46001	Abs46001 Human liv
c 502	16	1.0	129	6	ABS20593	Abs20593 Human gen
c 503	16	1.0	140	6	ABK39354	Abk39354 DNA encod
c 504	16	1.0	140	8	ACA11683	Aca11683 Human lun
c 505	16	1.0	140	8	ACA02869	Aca02869 Lung canc
c 506	16	1.0	140	10	ADH46911	Adh46911 Human lun
507	16	1.0	144	4	ABA71779	Aba71779 Human foe
508	16	1.0	144	4	AAI52114	Aai52114 Probe #20
509	16	1.0	144	4	AAK46208	Aak46208 Human bon
510	16	1.0	144	4	AAK20148	Aak20148 Human bra
511	16	1.0	144	4	ABS45927	Abs45927 Human liv
512	16	1.0	144	6	ABS20519	Abs20519 Human gen
c 513	16	1.0	148	3	AAC27928	Aac27928 Human sec
c 514	16	1.0	156	6	ABS17802	Abs17802 Human gen
515	16	1.0	181	4	AAL25447	Aal25447 Human bre
516	16	1.0	194	4	AAL16604	Aal16604 Human bre
c 517	16	1.0	197	3	AAC60873	Aac60873 Human IRG
c 518	16	1.0	198	12	ACH92845	Ach92845 Human gen
519	16	1.0	199	2	AAX32750	Aax32750 Human DcR
520	16	1.0	200	2	AAV39190	Aav39190 Antifunga
c 521	16	1.0	204	12	ACH82417	Ach82417 Human gen
522	16	1.0	205	8	ABX47106	Abx47106 Bovine ES
523	16	1.0	206	2	AAQ11831	Aaq11831 17kD TNF
524	16	1.0	206	4	ABA66139	Aba66139 Human foe
525	16	1.0	206	4	AAI46323	Aai46323 Probe #15
526	16	1.0	206	4	ABS39875	Abs39875 Human liv
527	16	1.0	206	6	ABS14329	Abs14329 Human gen
528	16	1.0	210	3	AAC15423	Aac15423 Human sec
c 529	16	1.0	214	2	AAT24795	Aat24795 Human gen
c 530	16	1.0	215	8	ABX45137	Abx45137 Bovine ES
c 531	16	1.0	220	12	ACH88040	Ach88040 Human gen
532	16	1.0	229	3	AAC25837	Aac25837 Human sec

	533	16	1.0	234	10	ADH84057 Adh84057 Enterococ
	534	16	1.0	237	5	ADL40139 Adl40139 Human ova
	535	16	1.0	238	5	ABV20035 Abv20035 Human pro
c	536	16	1.0	239	8	ABX54854 Abx54854 Bovine ES
c	537	16	1.0	242	2	AAQ61034 Aaq61034 Human bra
	538	16	1.0	246	3	AAC16484 Aac16484 Human sec
c	539	16	1.0	249	8	ABV93957 Abv93957 Human col
	540	16	1.0	250	2	AAV39187 Alfalfa p
	541	16	1.0	250	5	ADI74794 Adi74794 Human ova
	542	16	1.0	250	5	ADI68428 Adi68428 Human ova
c	543	16	1.0	252	2	AAT40856 Aat40856 Serine pr
c	544	16	1.0	252	2	AAT92853 Aat92853 Flea sali
c	545	16	1.0	252	2	AAV73401 Aav73401 Flea sali
c	546	16	1.0	252	4	AAC90864 Aac90864 Flea seri
c	547	16	1.0	255	5	AAH81956 Aah81956 Rat diffe
	548	16	1.0	255	5	ADL40032 Adl40032 Human ova
	549	16	1.0	256	4	AAK81668 Aak81668 Human imm
	550	16	1.0	259	6	ABL71512 Abl71512 Corn tass
c	551	16	1.0	260	5	ABV58104 Abv58104 Human pro
c	552	16	1.0	261	8	ABX55958 Abx55958 Bovine ES
	553	16	1.0	268	4	AAI24580 Aai24580 Probe #14
	554	16	1.0	268	4	ABA69751 Aba69751 Human foe
	555	16	1.0	268	4	AAI49836 Aai49836 Probe #18
	556	16	1.0	268	4	ABA36646 Aba36646 Probe #15
	557	16	1.0	268	4	AAK43821 Aak43821 Human bon
	558	16	1.0	268	4	AAK17944 Aak17944 Human bra
	559	16	1.0	268	4	ABS43469 Abs43469 Human liv
	560	16	1.0	268	6	ABS18048 Abs18048 Human gen
	561	16	1.0	271	2	AAX32747 Aax32747 Human DcR
	562	16	1.0	273	4	AAL36127 Aal36127 Human mus
	563	16	1.0	273	4	AAL36128 Aal36128 Human mus
	564	16	1.0	273	8	ABX59116 Abx59116 cDNA enco
	565	16	1.0	273	8	ABX59115 Abx59115 cDNA enco
	566	16	1.0	273	12	ADJ29866 Adj29866 Human mus
	567	16	1.0	273	12	ADJ29865 Adj29865 Human mus
	568	16	1.0	277	2	AAX32749 Aax32749 Human DcR
	569	16	1.0	277	5	ABV16923 Abv16923 Human pro
	570	16	1.0	278	5	ADL40030 Adl40030 Human ova
	571	16	1.0	282	12	ADL02521 Adl02521 DNA encod
	572	16	1.0	283	2	AAX32752 Aax32752 Human DcR
	573	16	1.0	287	3	AAC24946 Aac24946 Human sec
	574	16	1.0	290	5	ADI74793 Adi74793 Human ova
	575	16	1.0	290	5	ADI68427 Adi68427 Human ova
c	576	16	1.0	295	8	ABX52749 Abx52749 Bovine ES
c	577	16	1.0	297	10	ADC90461 Adc90461 E. faeciu
	578	16	1.0	304	5	ADL40031 Adl40031 Human ova
	579	16	1.0	305	4	AAH73192 Aah73192 Human cer
	580	16	1.0	306	4	AAH70506 Aah70506 Human cer
	581	16	1.0	312	5	ADI68418 Adi68418 Human ova
	582	16	1.0	312	5	ADI74784 Adi74784 Human ova
	583	16	1.0	317	5	ADI74834 Adi74834 Human ova
	584	16	1.0	317	5	ADI68468 Adi68468 Human ova
	585	16	1.0	322	5	ADI74816 Adi74816 Human ova
	586	16	1.0	322	5	ADI68450 Adi68450 Human ova
	587	16	1.0	324	5	ADI68481 Adi68481 Human ova
	588	16	1.0	324	5	ADI74846 Adi74846 Human ova
	589	16	1.0	325	5	ADL39996 Adl39996 Human ova
	590	16	1.0	328	5	ADI76827 Adi76827 Human ova
	591	16	1.0	328	5	ADI70502 Adi70502 Human ova
	592	16	1.0	329	5	ABA17354 Aba17354 Human ner
	593	16	1.0	331	4	AAH69766 Aah69766 Human cer
c	594	16	1.0	336	5	AAS81434 Aas81434 DNA encod
c	595	16	1.0	337	4	AAK70776 Aak70776 Human imm
c	596	16	1.0	339	11	ADO51600 Ado51600 Human TAG
c	597	16	1.0	340	4	AAS38159 Aas38159 Novel hum
	598	16	1.0	341	5	ABA12330 Aba12330 Human ner
	599	16	1.0	344	5	ADI74858 Adi74858 Human ova
	600	16	1.0	344	5	ADI68493 Adi68493 Human ova
	601	16	1.0	347	5	ADI74878 Adi74878 Human ova
	602	16	1.0	347	5	ADI68514 Adi68514 Human ova
	603	16	1.0	350	5	ADI68558 Adi68558 Human ova
	604	16	1.0	350	5	ADI74922 Adi74922 Human ova
	605	16	1.0	351	4	AAI89834 Aai89834 Human pol
	606	16	1.0	352	5	ADI68463 Adi68463 Human ova
	607	16	1.0	352	5	ADI74829 Adi74829 Human ova
	608	16	1.0	353	3	AAA32070 Aaa32070 Plant mic
	609	16	1.0	353	4	AAI80014 Aai80014 Human pol
	610	16	1.0	353	5	ADL40115 Adl40115 Human ova
	611	16	1.0	355	5	ABV02280 Abv02280 Human pro
	612	16	1.0	355	5	ADI68403 Adi68403 Human ova
	613	16	1.0	355	5	ADI74769 Adi74769 Human ova
	614	16	1.0	355	6	ABK45916 Abk45916 cDNA enco
	615	16	1.0	356	5	ADI74821 Adi74821 Human ova
	616	16	1.0	356	5	ADI68455 Adi68455 Human ova
c	617	16	1.0	357	4	AAL36451 Aal36451 Human mus
	618	16	1.0	357	5	ADL40094 Adl40094 Human ova
c	619	16	1.0	357	8	ABX59439 Abx59439 cDNA enco
c	620	16	1.0	357	12	ADJ30189 Adj30189 Human mus
	621	16	1.0	360	5	ADI74865 Adi74865 Human ova
	622	16	1.0	360	5	ADI68501 Adi68501 Human ova
c	623	16	1.0	361	12	ADL11299 Adl11299 Cat flea
	624	16	1.0	361	12	ADP92942 Adp92942 Cotton ex
	625	16	1.0	362	5	ADL40060 Adl40060 Human ova
	626	16	1.0	363	5	ADI74879 Adi74879 Human ova
	627	16	1.0	363	5	ADI68515 Adi68515 Human ova
c	628	16	1.0	364	9	ACH31759 Ach31759 Human bon
	629	16	1.0	365	5	ADL40116 Adl40116 Human ova
	630	16	1.0	369	5	ADL42063 Adl42063 Human ova
	631	16	1.0	369	5	ADI68560 Adi68560 Human ova
	632	16	1.0	369	5	ADI74924 Adi74924 Human ova
	633	16	1.0	370	5	ADI68562 Adi68562 Human ova
	634	16	1.0	370	5	ADI74926 Adi74926 Human ova
	635	16	1.0	372	4	AAL14631 Aal14631 Human bre
	636	16	1.0	373	5	ADL40083 Adl40083 Human ova
c	637	16	1.0	375	4	AAS23971 Aas23971 Human ova
c	638	16	1.0	375	4	AAS25307 Aas25307 Human ova
	639	16	1.0	378	5	ADI68528 Adi68528 Human ova
	640	16	1.0	378	5	ADI74892 Adi74892 Human ova
	641	16	1.0	381	4	AAS50654 Aas50654 Staphyloc
	642	16	1.0	381	4	AAS50738 Aas50738 Staphyloc
	643	16	1.0	381	8	ACA17939 Aca17939 Prokaryot
	644	16	1.0	381	8	ACA18017 Aca18017 Prokaryot
	645	16	1.0	386	5	ADI68458 Adi68458 Human ova
	646	16	1.0	386	5	ADI74824 Adi74824 Human ova
c	647	16	1.0	387	5	ABV13467 Abv13467 Human pro
	648	16	1.0	387	5	ADI68422 Adi68422 Human ova
	649	16	1.0	387	5	ADI74921 Adi74921 Human ova
	650	16	1.0	387	5	ADI74788 Adi74788 Human ova
	651	16	1.0	387	5	ADI68557 Adi68557 Human ova
c	652	16	1.0	387	6	ABQ91493 M. capsul
	653	16	1.0	390	5	ADI74866 Adi74866 Human ova
	654	16	1.0	390	5	ADI68502 Adi68502 Human ova
c	655	16	1.0	390	8	ABX41411 Bovine ES
c	656	16	1.0	390	10	ADB51050 Adb51050 Primary r
	657	16	1.0	393	3	AAC56280 Aac56280 Pinus rad
	658	16	1.0	393	12	ADK16186 Adk16186 Nanoarcha
	659	16	1.0	394	5	ADI68385 Adi68385 Human ova
	660	16	1.0	394	5	ADI74873 Adi74873 Human ova
	661	16	1.0	394	5	ADI74751 Adi74751 Human ova
	662	16	1.0	394	5	ADI68509 Adi68509 Human ova
	663	16	1.0	396	5	AAF64828 Aaf64828 Novel hum
	664	16	1.0	397	2	AAX07227 Aax07227 Human tum
c	665	16	1.0	397	3	AAH30252 Aah30252 Human col
	666	16	1.0	397	5	ADL40006 Adl40006 Human ova
c	667	16	1.0	398	4	AAH98237 Aah98237 Human EST
c	668	16	1.0	399	9	ACH20610 Ach20610 Human adu
	669	16	1.0	400	5	ADL40109 Adl40109 Human ova
c	670	16	1.0	400	6	ABL66985 Abl66985 Thyroid c
c	671	16	1.0	400	6	ABL68174 Abl68174 Kidney ca
	672	16	1.0	401	5	ADI68382 Adi68382 Human ova
	673	16	1.0	401	5	ADI74748 Adi74748 Human ova
c	674	16	1.0	402	5	ABV45856 Abv45856 Human pro
	675	16	1.0	403	5	ADI74809 Adi74809 Human ova
	676	16	1.0	403	5	ADI68443 Adi68443 Human ova
	677	16	1.0	404	5	ADL40021 Adl40021 Human ova
	678	16	1.0	404	5	ADI68533 Adi68533 Human ova

	679	16	1.0	404	5	ADI74897 Adi74897 Human ova
	680	16	1.0	405	5	ADI68466 Adi68466 Human ova
	681	16	1.0	405	5	ADI74832 Adi74832 Human ova
c	682	16	1.0	406	5	ABV55043 Abv55043 Human pro
	683	16	1.0	406	5	ADI74765 Adi74765 Human ova
	684	16	1.0	406	5	ADI68399 Adi68399 Human ova
	685	16	1.0	407	5	ADI68491 Adi68491 Human ova
	686	16	1.0	407	5	ADI74872 Adi74872 Human ova
	687	16	1.0	407	5	ADI74856 Adi74856 Human ova
	688	16	1.0	407	5	ADI68508 Adi68508 Human ova
	689	16	1.0	407	8	ABX35766 Abx35766 Bovine ES
	690	16	1.0	407	10	ACD94192 Acd94192 Human col
	691	16	1.0	409	5	ADI68555 Adi68555 Human ova
	692	16	1.0	409	5	ADI68400 Adi68400 Human ova
	693	16	1.0	409	5	ADI74919 Adi74919 Human ova
	694	16	1.0	409	5	ADI74766 Adi74766 Human ova
	695	16	1.0	410	5	ABV32594 Abv32594 Human pro
	696	16	1.0	410	5	ABV41519 Abv41519 Human pro
	697	16	1.0	410	5	ADI68473 Adi68473 Human ova
	698	16	1.0	410	5	ADI74838 Adi74838 Human ova
c	699	16	1.0	411	12	ACH71178 Ach71178 Human gen
	700	16	1.0	412	9	ACH19279 Ach19279 Human adu
c	701	16	1.0	413	5	AAS84687 Aas84687 DNA encod
	702	16	1.0	413	5	ADI74826 Adi74826 Human ova
	703	16	1.0	413	5	ADI68460 Adi68460 Human ova
c	704	16	1.0	414	5	ABV43439 Abv43439 Human pro
c	705	16	1.0	414	5	ABV34583 Abv34583 Human pro
	706	16	1.0	416	5	ADI68480 Adi68480 Human ova
	707	16	1.0	416	5	ADI68530 Adi68530 Human ova
	708	16	1.0	416	5	ADI74894 Adi74894 Human ova
	709	16	1.0	416	5	ADI74845 Adi74845 Human ova
c	710	16	1.0	417	4	AAL37113 Aal37113 Human mus
c	711	16	1.0	417	8	ABX60101 Abx60101 cDNA enco
c	712	16	1.0	417	12	ADJ30851 Adj30851 Human mus
	713	16	1.0	418	5	ADL40161 Adl40161 Human ova
	714	16	1.0	418	5	ADI74907 Adi74907 Human ova
	715	16	1.0	418	5	ADI74901 Adi74901 Human ova
	716	16	1.0	418	5	ADI68543 Adi68543 Human ova
	717	16	1.0	418	5	ADI68537 Adi68537 Human ova
	718	16	1.0	420	5	ADI68409 Adi68409 Human ova
	719	16	1.0	420	5	ADL38810 Adl38810 Human ova
	720	16	1.0	420	5	ADL38811 Adl38811 Human ova
	721	16	1.0	420	5	ADI68511 Adi68511 Human ova
	722	16	1.0	420	5	ADI74775 Adi74775 Human ova
	723	16	1.0	420	5	ADI74875 Adi74875 Human ova
	724	16	1.0	420	6	ABS69513 Abs69513 Novel mur
	725	16	1.0	421	5	ADI68496 Adi68496 Human ova
	726	16	1.0	421	5	ADL40063 Adl40063 Human ova
	727	16	1.0	421	5	ADI68471 Adi68471 Human ova
	728	16	1.0	421	9	ACH29641 Ach29641 Human tes
	729	16	1.0	423	5	ADL40163 Adl40163 Human ova
	730	16	1.0	424	4	AAS49850 Aas49850 Staphyloc
c	731	16	1.0	424	4	ABL17993 Abl17993 Drosophil
	732	16	1.0	424	8	ACA17118 Aca17118 Prokaryot
	733	16	1.0	425	5	ADI74852 Adi74852 Human ova
	734	16	1.0	425	5	ADI68487 Adi68487 Human ova
	735	16	1.0	425	10	ADF80283 Adf80283 Leukaemia
	736	16	1.0	427	5	ADL40110 Adl40110 Human ova
	737	16	1.0	427	5	ADL40095 Adl40095 Human ova
	738	16	1.0	427	5	ADL40093 Adl40093 Human ova
	739	16	1.0	428	5	ADL40066 Adl40066 Human ova
	740	16	1.0	430	5	ABV46718 Abv46718 Human pro
	741	16	1.0	430	5	ADI68526 Adi68526 Human ova
	742	16	1.0	430	5	ADI68519 Adi68519 Human ova
	743	16	1.0	430	5	ADI74883 Adi74883 Human ova
	744	16	1.0	430	5	ADI74890 Adi74890 Human ova
	745	16	1.0	432	4	AAL13682 Aal13682 Human bre
	746	16	1.0	433	5	ADI74803 Adi74803 Human ova
	747	16	1.0	433	5	ADI68437 Adi68437 Human ova
	748	16	1.0	433	5	ADI74840 Adi74840 Human ova
	749	16	1.0	433	5	ADI68475 Adi68475 Human ova
	750	16	1.0	434	5	ADL40071 Adl40071 Human ova
c	751	16	1.0	436	8	ABX46922 Abx46922 Bovine ES
	752	16	1.0	437	5	ADI68479 Adi68479 Human ova
	753	16	1.0	437	5	ADI74844 Adi74844 Human ova
	754	16	1.0	437	5	ADI74849 Adi74849 Human ova
	755	16	1.0	437	5	ADI68484 Adi68484 Human ova
	756	16	1.0	437	5	ADL40134 Adl40134 Human ova
	757	16	1.0	439	5	ABV11449 Abv11449 Human pro
	758	16	1.0	440	9	ACH19597 Ach19597 Human adu
c	759	16	1.0	441	5	AAS34277 Aas34277 Human cDN
	760	16	1.0	441	5	ADI68516 Adi68516 Human ova
	761	16	1.0	441	5	ADI74880 Adi74880 Human ova
c	762	16	1.0	443	4	AAL36260 Aal36260 Human mus
	763	16	1.0	443	5	ADI74817 Adi74817 Human ova
	764	16	1.0	443	5	ADI68451 Adi68451 Human ova
c	765	16	1.0	443	8	ABX59248 Abx59248 cDNA enco
c	766	16	1.0	443	12	ADJ29998 Adj29998 Human mus
	767	16	1.0	446	5	ADL40138 Adl40138 Human ova
	768	16	1.0	447	5	ADL40112 Adl40112 Human ova
	769	16	1.0	447	9	ACH24778 Ach24778 Human adu
	770	16	1.0	448	5	ADL40058 Adl40058 Human ova
	771	16	1.0	449	5	ADL40053 Adl40053 Human ova
	772	16	1.0	449	9	ACH27330 Ach27330 Human adu
	773	16	1.0	451	5	ADI68531 Adi68531 Human ova
	774	16	1.0	451	5	ADI74895 Adi74895 Human ova
	775	16	1.0	452	4	ABA59262 Aba59262 Human foe
	776	16	1.0	452	4	AAI39053 Aai39053 Probe #77
	777	16	1.0	452	4	AAK33259 Aak33259 Human bon
	778	16	1.0	452	4	AAK07474 Aak07474 Human bra
	779	16	1.0	452	4	ABS33009 Abs33009 Human liv
	780	16	1.0	452	6	ABS08091 Abs08091 Human gen
	781	16	1.0	452	12	ADP94175 Adp94175 Cotton ex
	782	16	1.0	453	5	ADL40131 Adl40131 Human ova
	783	16	1.0	454	5	ADL40117 Adl40117 Human ova
	784	16	1.0	454	5	ADI74889 Adi74889 Human ova
	785	16	1.0	454	5	ADI68525 Adi68525 Human ova
	786	16	1.0	454	5	ADL40102 Adl40102 Human ova
	787	16	1.0	455	5	ADI74749 Adi74749 Human ova
	788	16	1.0	455	5	ADI68383 Adi68383 Human ova
c	789	16	1.0	456	3	AAC09660 Aac09660 Human sec
	790	16	1.0	457	5	ADL40120 Adl40120 Human ova
	791	16	1.0	458	4	ABA53551 Aba53551 Human foe
	792	16	1.0	458	4	AAI33177 Aai33177 Probe #18
	793	16	1.0	458	4	AAK05149 Aak05149 Human bra
	794	16	1.0	458	4	ABS26852 Abs26852 Human liv
	795	16	1.0	458	4	ABS30412 Abs30412 Human liv
	796	16	1.0	458	5	ADI74813 Adi74813 Human ova
	797	16	1.0	458	5	ADL40103 Adl40103 Human ova
	798	16	1.0	458	5	ADI68447 Adi68447 Human ova
	799	16	1.0	458	6	ABS01804 Abs01804 Human gen
	800	16	1.0	459	2	AAX84621 Aax84621 Human TNF
	801	16	1.0	459	3	AAC63757 Aac63757 Human TNF
	802	16	1.0	459	12	ADL15577 Adl15577 Human NOD
	803	16	1.0	459	12	ADO21224 Ado21224 NOD2/CARD
c	804	16	1.0	460	9	ACH29129 Ach29129 Human adu
	805	16	1.0	460	12	ADL15575 Adl15575 Human NOD
	806	16	1.0	460	12	ADL15584 Adl15584 Human NOD
	807	16	1.0	460	12	ADL15582 Adl15582 Human NOD
	808	16	1.0	460	12	ADO21229 Ado21229 NOD2/CARD
	809	16	1.0	460	12	ADO21231 Ado21231 NOD2/CARD
	810	16	1.0	460	12	ADO21222 Ado21222 NOD2/CARD
	811	16	1.0	461	5	ADL40061 Adl40061 Human ova
	812	16	1.0	462	9	ACH34516 Ach34516 Human end
	813	16	1.0	462	12	ADL15576 Adl15576 Human NOD
	814	16	1.0	462	12	ADL15585 Adl15585 Human NOD
	815	16	1.0	462	12	ADO21223 Ado21223 NOD2/CARD
	816	16	1.0	462	12	ADO21232 Ado21232 NOD2/CARD
	817	16	1.0	463	5	ADL40016 Adl40016 Human ova
	818	16	1.0	463	5	ADI68421 Adi68421 Human ova
	819	16	1.0	463	5	ADI74787 Adi74787 Human ova
	820	16	1.0	463	5	ADL40025 Adl40025 Human ova
	821	16	1.0	463	12	ADL15586 Adl15586 Human NOD
	822	16	1.0	463	12	ADO21233 Ado21233 NOD2/CARD
	823	16	1.0	464	5	ADI74779 Adi74779 Human ova
	824	16	1.0	464	5	ADI68413 Adi68413 Human ova

	825	16	1.0	464	9	ACH28090 Ach28090 Human adu
	826	16	1.0	465	5	ADI68436 Adi68436 Human ova
	827	16	1.0	465	5	ADI74802 Adi74802 Human ova
c	828	16	1.0	465	10	ADK55562 Adk55562 Plant DNA
	829	16	1.0	466	5	ADL41915 Adl41915 Human ova
	830	16	1.0	466	12	ADL15580 Adl15580 Human NOD
	831	16	1.0	466	12	ADL15581 Adl15581 Human NOD
	832	16	1.0	466	12	ADO21228 Ado21228 NOD2/CARD
	833	16	1.0	466	12	ADO21227 Ado21227 NOD2/CARD
	834	16	1.0	467	5	ADL40106 Adl40106 Human ova
	835	16	1.0	467	12	ADL15578 Adl15578 Human NOD
	836	16	1.0	467	12	ADL15583 Adl15583 Human NOD
	837	16	1.0	467	12	ADL15579 Adl15579 Human NOD
	838	16	1.0	467	12	ADO21226 Ado21226 NOD2/CARD
	839	16	1.0	467	12	ADO21225 Ado21225 NOD2/CARD
	840	16	1.0	467	12	ADO21230 Ado21230 NOD2/CARD
c	841	16	1.0	469	4	ABA08415 Aba08415 Human sn-
	842	16	1.0	469	5	ADI68440 Adi68440 Human ova
	843	16	1.0	469	5	ADI74806 Adi74806 Human ova
	844	16	1.0	470	4	AAI16133 Aai16133 Probe #60
	845	16	1.0	470	4	ABA58731 Aba58731 Human foe
	846	16	1.0	470	4	AAI38409 Aai38409 Probe #70
	847	16	1.0	470	4	ABA27688 Aba27688 Probe #61
	848	16	1.0	470	4	AAK32589 Aak32589 Human bon
	849	16	1.0	470	4	AAK06867 Aak06867 Human bra
	850	16	1.0	470	4	ABS32300 Abs32300 Human liv
	851	16	1.0	470	6	ABS07378 Abs07378 Human gen
	852	16	1.0	471	5	ADI74815 Adi74815 Human ova
	853	16	1.0	471	5	ADI68449 Adi68449 Human ova
	854	16	1.0	471	9	ACH24722 Ach24722 Human adu
	855	16	1.0	472	5	ADL40081 Adl40081 Human ova
	856	16	1.0	474	5	ADL40974 Adl40974 Human ova
	857	16	1.0	475	5	ADI68472 Adi68472 Human ova
	858	16	1.0	475	5	ADL40054 Adl40054 Human ova
	859	16	1.0	475	5	ADI74837 Adi74837 Human ova
	860	16	1.0	476	5	ADL39985 Adl39985 Human ova
	861	16	1.0	477	9	ACH15881 Ach15881 Human adu
	862	16	1.0	478	5	ADI74912 Adi74912 Human ova
	863	16	1.0	478	5	ADI68548 Adi68548 Human ova
	864	16	1.0	479	5	ADL40075 Adl40075 Human ova
	865	16	1.0	480	2	AAQ62691 Aaq62691 HCV antig
	866	16	1.0	480	3	AAA69750 Aaa69750 Human ova
c	867	16	1.0	480	4	AAK33403 Aak33403 Human bon
	868	16	1.0	480	5	ADL40003 Adl40003 Human ova
	869	16	1.0	480	6	ABN72644 Abn72644 Ovarian c
	870	16	1.0	480	9	ACH13921 Ach13921 Human adu
	871	16	1.0	480	9	ACH26388 Ach26388 Human adu
	872	16	1.0	480	9	ADA08809 Ada08809 Human ova
	873	16	1.0	480	10	ADF08556 Adf08556 cDNA enco
	874	16	1.0	480	10	ADG46304 Adg46304 Human ova
	875	16	1.0	480	12	ADI30096 Adi30096 M. methyl
c	876	16	1.0	482	9	ACH34432 Ach34432 Human end
c	877	16	1.0	482	10	ADD32923 Add32923 Human mit
c	878	16	1.0	483	2	AAV89019 Aav89019 EST clone
	879	16	1.0	483	5	ADI74869 Adi74869 Human ova
	880	16	1.0	483	5	ADL40002 Adl40002 Human ova
	881	16	1.0	483	5	ADI68505 Adi68505 Human ova
c	882	16	1.0	484	6	ABS05302 Abs05302 Human gen
	883	16	1.0	485	2	AAQ26994 Aaq26994 HCV gene
	884	16	1.0	485	2	AAV05567 Aav05567 DNA assoc
	885	16	1.0	485	9	ACH34755 Ach34755 Human end
c	886	16	1.0	486	4	AAL12761 Aal12761 Human bre
c	887	16	1.0	486	4	AAK93804 Aak93804 Human cDN
c	888	16	1.0	486	4	AAK91781 Aak91781 Human cDN
	889	16	1.0	486	5	ADL40085 Adl40085 Human ova
c	890	16	1.0	486	12	ADL28208 Adl28208 5' end of
c	891	16	1.0	486	12	ADL30231 Adl30231 3' end of
	892	16	1.0	487	5	ADL40046 Adl40046 Human ova
c	893	16	1.0	487	9	ACH33337 Ach33337 Human end
	894	16	1.0	488	6	ABV97729 Abv97729 Human pan
	895	16	1.0	489	5	ADL40156 Adl40156 Human ova
	896	16	1.0	490	2	AAV39186 Aav39186 Antifunga
	897	16	1.0	490	5	ADL40039 Adl40039 Human ova
	898	16	1.0	490	5	ADL40077 Adl40077 Human ova
	899	16	1.0	491	2	AAX32745 Aax32745 Human DcR
	900	16	1.0	491	5	ADI68551 Adi68551 Human ova
	901	16	1.0	491	5	ADI74915 Adi74915 Human ova
	902	16	1.0	492	5	ADL40129 Adl40129 Human ova
	903	16	1.0	493	5	ADL40127 Adl40127 Human ova
	904	16	1.0	495	3	AAC75463 Aac75463 Human ORF
	905	16	1.0	495	3	AAC53446 Aac53446 Arabidops
	906	16	1.0	495	5	ADL40126 Adl40126 Human ova
c	907	16	1.0	496	4	ABA59322 Aba59322 Human foe
c	908	16	1.0	496	4	AAI39123 Aai39123 Probe #78
c	909	16	1.0	496	4	AAK33336 Aak33336 Human bon
c	910	16	1.0	496	4	AAK07540 Aak07540 Human bra
c	911	16	1.0	496	4	ABS33089 Abs33089 Human liv
c	912	16	1.0	496	6	ABS08171 Abs08171 Human gen
c	913	16	1.0	496	9	ACH39708 Ach39708 Human foe
	914	16	1.0	496	9	ACH33892 Ach33892 Human end
	915	16	1.0	497	5	ADI68541 Adi68541 Human ova
	916	16	1.0	497	5	ADI74905 Adi74905 Human ova
	917	16	1.0	497	12	ADL15574 Adl15574 Human NOD
	918	16	1.0	497	12	ADO21221 Ado21221 NOD2/CARD
c	919	16	1.0	499	4	AAK92835 Aak92835 Human cDN
c	920	16	1.0	499	12	ADL29262 Adl29262 3' end of
	921	16	1.0	500	5	ADL40132 Adl40132 Human ova
c	922	16	1.0	500	12	ACH68717 Ach68717 Human gen
	923	16	1.0	501	5	ABA14279 Aba14279 Human ner
	924	16	1.0	501	10	ABX07706 Abx07706 S. pneumo
c	925	16	1.0	502	5	AAH82536 Aah82536 Human ova
	926	16	1.0	502	5	ADI74920 Adi74920 Human ova
	927	16	1.0	502	5	ADI68556 Adi68556 Human ova
	928	16	1.0	502	5	ADL40082 Adl40082 Human ova
c	929	16	1.0	503	3	AAC99924 Aac99924 Human sec
c	930	16	1.0	503	6	ABQ60717 Abq60717 Human col
	931	16	1.0	504	4	AAL11095 Aal11095 Human bre
	932	16	1.0	504	5	ADI74811 Adi74811 Human ova
	933	16	1.0	504	5	ADI68381 Adi68381 Human ova
	934	16	1.0	504	5	ADI74747 Adi74747 Human ova
	935	16	1.0	504	5	ADL40076 Adl40076 Human ova
	936	16	1.0	504	5	ADI68445 Adi68445 Human ova
	937	16	1.0	505	5	ADI74847 Adi74847 Human ova
	938	16	1.0	505	5	ADI68482 Adi68482 Human ova
	939	16	1.0	506	5	ADL40043 Adl40043 Human ova
	940	16	1.0	507	2	AAV39195 Aav39195 Antifunga
	941	16	1.0	507	5	ADI74848 Adi74848 Human ova
	942	16	1.0	507	5	ADI68412 Adi68412 Human ova
	943	16	1.0	507	5	ADI68483 Adi68483 Human ova
	944	16	1.0	507	5	ADI74778 Adi74778 Human ova
	945	16	1.0	508	5	ADL40050 Adl40050 Human ova
c	946	16	1.0	508	12	ACH67903 Ach67903 Human gen
	947	16	1.0	509	5	ADL40086 Adl40086 Human ova
	948	16	1.0	509	5	ADL40088 Adl40088 Human ova
	949	16	1.0	510	5	ADI68545 Adi68545 Human ova
	950	16	1.0	510	5	ADL40070 Adl40070 Human ova
	951	16	1.0	510	5	ADI74909 Adi74909 Human ova
	952	16	1.0	511	5	ADL40073 Adl40073 Human ova
	953	16	1.0	513	5	ADL40089 Adl40089 Human ova
	954	16	1.0	513	5	ADL40159 Adl40159 Human ova
	955	16	1.0	513	5	ADI68405 Adi68405 Human ova
	956	16	1.0	513	5	ADI74771 Adi74771 Human ova
	957	16	1.0	514	3	AAC36860 Aac36860 Arabidops
	958	16	1.0	516	5	ADL40074 Adl40074 Human ova
	959	16	1.0	517	5	ADL40040 Adl40040 Human ova
	960	16	1.0	517	5	ADL40052 Adl40052 Human ova
	961	16	1.0	519	5	ADI68444 Adi68444 Human ova
	962	16	1.0	519	5	ADI74810 Adi74810 Human ova
	963	16	1.0	521	5	ADI68439 Adi68439 Human ova
	964	16	1.0	521	5	ADL40084 Adl40084 Human ova
	965	16	1.0	521	5	ADI74805 Adi74805 Human ova
c	966	16	1.0	522	12	ACH79145 Ach79145 Human gen
	967	16	1.0	523	5	ADL40012 Adl40012 Human ova
	968	16	1.0	524	5	ADI74773 Adi74773 Human ova
	969	16	1.0	524	5	ADI74851 Adi74851 Human ova
	970	16	1.0	524	5	ADI68407 Adi68407 Human ova

971	16	1.0	524	5	ADI74839	Adi74839 Human ova
972	16	1.0	524	5	ADI68486	Adi68486 Human ova
973	16	1.0	524	5	ADI68474	Adi68474 Human ova
974	16	1.0	525	5	ADL40069	Adl40069 Human ova
975	16	1.0	525	5	ADI74764	Adi74764 Human ova
976	16	1.0	525	5	ADI68398	Adi68398 Human ova
977	16	1.0	527	5	ADL39986	Adl39986 Human ova
c 978	16	1.0	527	6	ABQ60704	Abq60704 Human col
979	16	1.0	528	6	ABV88075	Abv88075 Human col
980	16	1.0	529	5	ADL41887	Adl41887 Human ova
c 981	16	1.0	529	6	ABQ59849	Abq59849 Human col
c 982	16	1.0	529	6	ABL83482	Abl83482 Human ova
983	16	1.0	529	6	ABL37264	Abl37264 Human col
984	16	1.0	530	2	AAQ26995	Aaq26995 HCV gene
985	16	1.0	530	2	AAV05568	Aav05568 DNA assoc
986	16	1.0	531	3	AAA69695	Aaa69695 Human ova
987	16	1.0	531	6	ABN72589	Abn72589 Ovarian c
c 988	16	1.0	531	6	ABK79052	Abk79052 Bacillus
989	16	1.0	531	9	ADA08754	Ada08754 Human ova
990	16	1.0	531	10	ADF08501	Adf08501 cDNA enco
991	16	1.0	531	10	ADG46249	Adg46249 Human ova
992	16	1.0	533	5	ADI74836	Adi74836 Human ova
993	16	1.0	533	5	ADI68470	Adi68470 Human ova
994	16	1.0	536	5	ADL39988	Adl39988 Human ova
995	16	1.0	537	4	AAK87319	Aak87319 Human imm
996	16	1.0	538	5	ADI74857	Adi74857 Human ova
997	16	1.0	538	5	ADI68492	Adi68492 Human ova
c 998	16	1.0	542	3	AAC94996	Aac94996 Cat flea
c 999	16	1.0	546	4	ABA59802	Aba59802 Human foe
c1000	16	1.0	546	4	AAK33949	Aak33949 Human bon

ALIGNMENTS

RESULT 1
AAS01082
ID AAS01082 standard; DNA; 1641 BP.
XX
AC AAS01082;
XX
DT 31-MAY-2001 (first entry)
XX
DE Arabidopsis thaliana sterol acyltransferase LCAT2 DNA.
XX
KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW nutritional supplement; dairy product; food product; salad dressing; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1. .1641
FT /*tag= a
FT /product= "LCAT2"
XX
PN WO200116308-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023863.
XX
PR 30-AUG-1999; 99US-0152493P.
XX
PA (MONS) MONSANTO CO.
XX
PI Lassner M, Van Eenennaam A;
XX
DR WPI; 2001-169010/17.
DR P-PSDB; AAU00459.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT -like polypeptides, for modifying the sterol content and oil production
PT of plants.
XX
PS Claim 5; Page 77; 127pp; English.
XX
CC The present sequence encodes for Arabidopsis thaliana
CC lecithin:cholesterol acyltransferase-like 2 (LCAT2). Several novel
CC polynucleotides encoding the plant sterol acyltransferases LCAT
CC (AAS001081-AAS01104, AAS01341) and ACAT (acyl CoA:cholesterol
CC acyltransferase-like; AAS01311-AAS01319) are described. A yeast LCAT
CC related open reading frame, LRO1 gene sequence (AAS01342), and a rat ACAT
CC (AAS01105) cDNA sequence are also described. The polynucleotides encoding
CC LCAT or ACAT are used to produce LCAT or ACAT polypeptides. They can also
CC be used in a recombinant construct to transform a host cell (preferably
CC of a plant) or a plant. The recombinant construct is used to increase or
CC decrease the sterol content of the host cell or plant. It can be used to
CC alter oil production of the cell or plant, preferably by increasing it.
CC The oil of the plant or the plant itself is used as a food product, or as
CC nutritional or dietary supplements, or in pharmaceutical compositions for
CC lowering cholesterol. The oil can be used in foods e.g. margarine,
CC butter, cooking oil, and dressings e.g. salad dressings, mayonnaise,
CC cheese, processed meat, pasta, sauces, cereals, desserts, dips, chips,
CC baked goods, pastries, cookies, snack bars, confections, chocolates, and
CC beverages. The alteration in sterol content and/or composition can also
CC provide a plant with tolerance to stress and insect damage
XX
SQ Sequence 1641 BP; 438 A; 355 C; 378 G; 470 T; 0 U; 0 Other;

Query Match 100.0%; Score 1641; DB 5; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420

Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480

Qy        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540

Qy        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600

Qy        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660

Qy        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720

Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780

Qy        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840

Qy        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900

Qy        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960

Qy        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140

Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200

Qy       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260

Qy       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320

Qy       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380

Qy       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440

Qy       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500

Qy       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560

Qy       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620

Qy       1621 CTTGATAAAAGTGGGTATTAA 1641
                    |||||||||||||||||||||
Db       1621 CTTGATAAAAGTGGGTATTAA 1641
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RESULT 2

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ADF47823
ID   ADF47823 standard; DNA; 1902 BP.
XX
AC   ADF47823;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Arabidopsis thaliana acyltransferase nucleotide sequence SEQ ID NO:8.
XX
KW   acyltransferase; enzyme; membrane-spanning region;
KW   active membrane independent acyltransferase; fatty acid ester;
KW   fatty acid thioester; triacylglycerol; diacylglycerol; monoacylglycerol;
KW   phospholipid; glycolipid; lysolipid; waxester; acylated carbohydrate;
KW   acylated amino acid; structured lipid; fat-soluble molecule; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO2003100044-A1.
XX
PD   04-DEC-2003.
XX
PF   28-MAY-2003; 2003WO-SE000870.
XX
PR   29-MAY-2002; 2002SE-00001581.
PR   29-MAY-2002; 2002US-0383889P.
PR   20-JAN-2003; 2003SE-00000142.
XX
PA   (SCAN-) SCANBI SCANDINAVIAN BIOTECHNOLOGY RES AB.
XX
PI   Dahlqvist A,  Ghosal A,  Lindqvist Y,  Banas A;
XX
DR   WPI; 2004-053268/05.
DR   P-PSDB; ADF47824.
XX
PT   New nucleotide sequence encoding an improved acyltransferase polypeptide,
PT   useful for producing structured lipids or fat-soluble molecules, in
PT   removing undesirable fat or in modifying lipids in animal or plant raw
PT   material.
XX
PS   Claim 5; SEQ ID NO 8; 91pp; English.
XX
CC   The present invention describes a nucleotide sequence (I) derived from a
CC   nucleotide sequence encoding an acyltransferase polypeptide comprising at
CC   least one membrane-spanning region. (I) encodes an improved active
CC   membrane independent acyltransferase polypeptide in which at least one
CC   amino acid residue of the membrane-spanning region has been deleted
CC   and/or substituted as compared to the original acyltransferase
CC   polypeptide, where the encoded active membrane independent
CC   acyltransferase polypeptide can produce fatty acid esters and/or fatty
CC   acid thioesters such as triacylglycerols, diacylglycerols,
CC   monoacylglycerols, phospholipids, glycolipids, lysolipids, waxesters,
CC   acylated carbohydrates and acylated amino acids. Also described: (1) a
CC   nucleotide sequence molecule (II) comprising at least one promoter region
CC   which functions in a host, where the promoter region is operably linked
CC   to at least one (I), which is operably linked to at least one non-
CC   translated region which functions in a host; (2) a vector comprising (II)
CC   ; (3) a host cell comprising (II) or the vector; (4) producing an
CC   improved active membrane independent acyltransferase polypeptide,
CC   comprising providing the above host cell and a growth medium preparing a
CC   host cell culture, culturing the host cell culture and harvesting the
CC   host cell culture and recovering the improved active membrane independent
CC   acyltransferase polypeptide; (5) a polypeptide obtained by the method in
CC   (4), where the polypeptide at least is an improved active membrane
CC   independent acyltransferase polypeptide; (6) an oligonucleotide
CC   specifically hybridising to (I) under stringent conditions; and (7) a kit
CC   comprising the above polypeptide and a stabiliser. The nucleic acid
CC   molecule (I) and the polypeptide are useful in producing structured
CC   lipids or fat-soluble molecules, in removing undesirable fat or in
CC   modifying lipids present in animal and plant raw material. The present
CC   sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 1902 BP; 516 A; 405 C; 444 G; 537 T; 0 U; 0 Other;
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  Query Match             83.8%;  Score 1375;  DB 12;  Length 1902;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1625;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTGCGGTGGCCGAACGGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420

Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTGAGTTTGGTGTAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480

Qy        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAACCAAATTGGAAGAGCGTGACCTTTACTTTCACAAGCTCAAGTTGACCTTTGAAACT 540

Qy        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTTTAAAACTCCGTGGCGGCCCTTCTATAGTATTTGCCCATTCAATGGGTAATAATGTC 600

Qy        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660

Qy        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTTGATCAGCATATCCATGCTTATTTCGCTGTTGGAGCTCCTCTTCTTGGTTCTGTTGAG 720

Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780

Qy        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGTTGTTGTCCAATTCTTTTGCGTCGTCATTGTGGCTTATGCCATTTTCAAAGAATTGC 840

Qy        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGGTGATAACACATTCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900

Qy        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960

Qy        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGGAATGTGGCCTCCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140

Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200

Qy       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260

Qy       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTATGAAACTGAA 1320

Qy       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GGTTCCCTCGTGTCAAGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGG 1380

Qy       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GATGAGACGGTACCCTATCATTCACTCTCTTGGTGCAAGAATTGGCTCGGACCTAAAGTT 1440

Qy       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AACATAACAATGGCTCCCCAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAAT 1500

Qy       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560

Qy       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620

Qy       1621 CTTGATAAAA 1630
              ||||||||||
Db       1621 CTTGATAAAA 1630
```

```
RESULT 3
AAC64438
ID   AAC64438 standard; DNA; 3896 BP.
XX
AC   AAC64438;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:11.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
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DR   WPI; 2000-665012/64.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 60-61; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the Arabidopsis
CC   thaliana PDAT genomic DNA
XX
SQ   Sequence 3896 BP; 1042 A; 725 C; 769 G; 1360 T; 0 U; 0 Other;

  Query Match             14.8%;  Score 243;  DB 3;  Length 3896;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-116;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAG 243
              |||
Db        241 AAG 243


RESULT 4
AAC64448
ID   AAC64448 standard; DNA; 3896 BP.
XX
AC   AAC64448;
XX
DT   12-FEB-2001  (first entry)
XX
DE   Arabidopsis thaliana PDAT genomic DNA SEQ ID NO:10b.
XX
KW   PDAT; phospholipid:diacylglycerol acyltransferase; triacylglycerol; TAG;
KW   EST; expressed sequence tag; fatty acid; oil content; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200060095-A2.
XX
PD   12-OCT-2000.
XX
PF   28-MAR-2000; 2000WO-EP002701.
XX
PR   01-APR-1999;   99EP-00106656.
PR   10-JUN-1999;   99EP-00111321.
PR   07-FEB-2000; 2000US-0180687P.
XX
PA   (BADI ) BASF PLANT SCI GMBH.
XX
PI   Dahlqvist A,  Stahl U,  Lenman M,  Banas A,  Ronne H,  Stymne S;
XX
DR   WPI; 2000-665012/64.
XX
PT   Phospholipid:diacylglycerol acyltransferase enzymes in the biosynthetic
PT   pathway for triacylglycerol production and DNAs encoding them, useful for
PT   producing triacylglycerol, or for transforming any cell or organism to
PT   increase oil content.
XX
PS   Claim 6; Page 95-96; 97pp; English.
XX
CC   The present invention describes an enzyme for catalysing (in an acyl-CoA-
CC   independent reaction) the transfer of fatty acids from phospholipids to
CC   diacylglycerol in the biosynthetic pathway for the production of
CC   triacylglycerol (TAG). The enzyme is designated as
CC   phospholipid:diacylglycerol acyltransferase (PDAT). The enzyme and the
CC   nucleotides encoding them are useful for producing TAG and/or TAG with
CC   uncommon fatty acids. The enzyme and the nucleotide are also useful for
CC   transforming any cell or organism in order to be expressed in this cell
CC   or organism and result in an altered, preferably increased oil content of
CC   this cell or organism. The present sequence represents the Arabidopsis
CC   thaliana PDAT genomic DNA
XX
SQ   Sequence 3896 BP; 1042 A; 733 C; 760 G; 1360 T; 0 U; 1 Other;

  Query Match             11.2%;  Score 183;  DB 3;  Length 3896;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-84;
  Matches  183;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1459 CAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGG 1518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3714 CAGCCAGAACACGATGGAAGCGACGTACATGTGGAACTAAATGTTGATCATGAGCATGGG 3773

Qy       1519 TCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAA 1578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3774 TCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAGTACATAACCTTTTATGAA 3833

Qy       1579 GACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAAAGTGGGTAT 1638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3834 GACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAGCTTGATAAAAGTGGGTAT 3893

Qy       1639 TAA 1641
              |||
Db       3894 TAA 3896


RESULT 5
AAS01322
ID   AAS01322 standard; DNA; 44 BP.
XX
AC   AAS01322;
XX
DT   31-MAY-2001  (first entry)
XX
DE   Arabidopsis thaliana LCAT2 coding sequence PCR primer #1.
XX
KW   Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW   acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW   nutritional supplement; dairy product; food product; salad dressing;
KW   PCR primer; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200116308-A2.
XX
PD   08-MAR-2001.
XX
PF   30-AUG-2000; 2000WO-US023863.
XX
PR   30-AUG-1999;   99US-0152493P.
XX
```

PA (MONS) MONSANTO CO.
XX
PI Lassner M, Van Eenennaam A;
XX
DR WPI; 2001-169010/17.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT -like polypeptides, for modifying the sterol content and oil production
PT of plants.
XX
PS Example 4; Page 36; 127pp; English.
XX
CC The present sequence for LCAT2 PCR primer #1 is used with PCR primer #2
CC (AAS01323) to amplify Arabidopsis thaliana lecithin:cholesterol
CC acyltransferase-like 2 (LCAT2). The PCR product is used to prepare an
CC expression construct. Several novel polynucleotides encoding the plant
CC sterol acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT
CC (acyl CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are
CC described. A yeast LCAT related open reading frame, LRO1 gene sequence
CC (AAS01342), and a rat ACAT (AAS01105) cDNA sequence are also described.
CC The polynucleotides encoding LCAT or ACAT are used to produce LCAT or
CC ACAT polypeptides. They can also be used in a recombinant construct to
CC transform a host cell (preferably of a plant) or a plant. The recombinant
CC construct is used to increase or decrease the sterol content of the host
CC cell or plant. It can be used to alter oil production of the cell or
CC plant, preferably by increasing it. The oil of the plant or the plant
CC itself is used as a food product, or as nutritional or dietary
CC supplements, or in pharmaceutical compositions for lowering cholesterol.
CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
CC cookies, snack bars, confections, chocolates, and beverages. The
CC alteration in sterol content and/or composition can also provide a plant
CC with tolerance to stress and insect damage
XX
SQ Sequence 44 BP; 13 A; 11 C; 14 G; 6 T; 0 U; 0 Other;

Query Match 1.6%; Score 27; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGAGCGAATTCGAAATCAGTAACG 27
||||||||||||||||||||||||||||
Db 18 ATGGGAGCGAATTCGAAATCAGTAACG 44

RESULT 6
AAS01323/c
ID AAS01323 standard; DNA; 40 BP.
XX
AC AAS01323;
XX
DT 31-MAY-2001 (first entry)
XX
DE Arabidopsis thaliana LCAT2 coding sequence PCR primer #2.
XX
KW Lecithin:cholesterol acyltransferase-like; LCAT; sterol acyltransferase;
KW acyl CoA:cholesterol acyltransferase-like; ACAT; plant oil; cooking oil;
KW nutritional supplement; dairy product; food product; salad dressing;
KW PCR primer; ss.
XX
OS Arabidopsis thaliana.
XX
PN WO200116308-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023863.
XX
PR 30-AUG-1999; 99US-0152493P.
XX
PA (MONS) MONSANTO CO.
XX
PI Lassner M, Van Eenennaam A;
XX
DR WPI; 2001-169010/17.
XX
PT New isolated nucleic acid encoding plant lecithin:cholesterol
PT acyltransferase-like or acyl (coenzyme A) CoA:cholesterol acyltransferase
PT -like polypeptides, for modifying the sterol content and oil production
PT of plants.
XX
PS Example 4; Page 36; 127pp; English.
XX
CC The present sequence for LCAT2 PCR primer #2 is used with PCR primer #1
CC (AAS01322) to amplify Arabidopsis thaliana lecithin:cholesterol
CC acyltransferase-like 2 (LCAT2). The PCR product is used to prepare an
CC expression construct. Several novel polynucleotides encoding the plant
CC sterol acyltransferases LCAT (AAS001081-AAS01104, AAS01341) and ACAT
CC (acyl CoA:cholesterol acyltransferase-like; AAS01311-AAS01319) are
CC described. A yeast LCAT related open reading frame, LRO1 gene sequence
CC (AAS01342), and a rat ACAT (AAS01105) cDNA sequence are also described.
CC The polynucleotides encoding LCAT or ACAT are used to produce LCAT or
CC ACAT polypeptides. They can also be used in a recombinant construct to
CC transform a host cell (preferably of a plant) or a plant. The recombinant
CC construct is used to increase or decrease the sterol content of the host
CC cell or plant. It can be used to alter oil production of the cell or
CC plant, preferably by increasing it. The oil of the plant or the plant
CC itself is used as a food product, or as nutritional or dietary
CC supplements, or in pharmaceutical compositions for lowering cholesterol.
CC The oil can be used in foods e.g. margarine, butter, cooking oil, and
CC dressings e.g. salad dressings, mayonnaise, cheese, processed meat,
CC pasta, sauces, cereals, desserts, dips, chips, baked goods, pastries,
CC cookies, snack bars, confections, chocolates, and beverages. The
CC alteration in sterol content and/or composition can also provide a plant
CC with tolerance to stress and insect damage
XX
SQ Sequence 40 BP; 9 A; 14 C; 6 G; 11 T; 0 U; 0 Other;

Query Match 1.6%; Score 26; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1616 GGGAGCTTGATAAAAGTGGGTATTAA 1641
||||||||||||||||||||||||||
Db 40 GGGAGCTTGATAAAAGTGGGTATTAA 15

RESULT 7
AAL06791/c
ID AAL06791 standard; DNA; 31140 BP.
XX
AC AAL06791;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 9479.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 9479; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a

```
CC   protein of the invention
XX
SQ   Sequence 31140 BP; 7333 A; 7322 C; 7497 G; 8988 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 20;  DB 4;  Length 31140;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 TGAAACTGCTTTAAAACTCC 553
              ||||||||||||||||||||
Db      25120 TGAAACTGCTTTAAAACTCC 25101


RESULT 8
ABA08065/c
ID   ABA08065 standard; DNA; 31140 BP.
XX
AC   ABA08065;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human ovarian and breast cancer associated polynucleotide SEQ ID NO 860.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155325-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001345.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
PR   17-NOV-2000; 2000US-0249210P.
PR   17-NOV-2000; 2000US-0249211P.
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PR   17-NOV-2000; 2000US-0249212P.
PR   17-NOV-2000; 2000US-0249213P.
PR   17-NOV-2000; 2000US-0249214P.
PR   17-NOV-2000; 2000US-0249215P.
PR   17-NOV-2000; 2000US-0249216P.
PR   17-NOV-2000; 2000US-0249217P.
PR   17-NOV-2000; 2000US-0249218P.
PR   17-NOV-2000; 2000US-0249244P.
PR   17-NOV-2000; 2000US-0249245P.
PR   17-NOV-2000; 2000US-0249264P.
PR   17-NOV-2000; 2000US-0249265P.
PR   17-NOV-2000; 2000US-0249297P.
PR   17-NOV-2000; 2000US-0249299P.
PR   17-NOV-2000; 2000US-0249300P.
PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
PR   08-DEC-2000; 2000US-0251868P.
PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-488786/53.
XX
PT   New isolated ovarian and/or breast cancer related nucleic acids and
PT   polypeptides, useful for diagnosing, treating and/or preventing human
PT   diseases and disorders, particularly ovarian and/or breast cancer.
XX
PS   Disclosure; SEQ ID NO 860; 577pp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA07454-ABA08224) and proteins
CC   (ABB10743-ABB10980) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC   the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC   ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC   breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC   disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC   anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC   multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC   ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC   infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections. Note: The sequence data for this patent did not form part of
CC   the printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 31140 BP; 7333 A; 7322 C; 7497 G; 8988 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 20;  DB 4;  Length 31140;
  Best Local Similarity   100.0%;  Pred. No. 24;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 TGAAACTGCTTTAAAACTCC 553
              ||||||||||||||||||||
Db      25120 TGAAACTGCTTTAAAACTCC 25101


RESULT 9
AAD58279
ID   AAD58279 standard; DNA; 226475 BP.
XX
AC   AAD58279;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human tumour suppressor gene, Lmt reverse complement DNA.
XX
KW   Tumour suppressor gene; Lmt; cancer; therapy; cytostatic; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003066869-A1.
XX
PD   14-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-AU000126.
XX
PR   07-FEB-2002; 2002AU-00000371.
XX
PA   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI   Cook WD,  Mccaw BJ;
XX
DR   WPI; 2003-646311/61.
XX
PT   New nucleic acid molecule, useful for screening a subject for the
PT   presence of an aberration in a gene encoding an LMT.
XX
PS   Claim 10; Page 233-299; 373pp; English.
XX
CC   The invention relates to novel tumour suppressor gene, referred to as
CC   Lmt. The invention also relates to the field of cancer therapy and cancer
CC   diagnostics. The nucleic acid molecule is useful for screening a subject
CC   for the presence of an aberration in a gene encoding an LMT. The present
CC   sequence is human Lmt reverse complement DNA
XX
SQ   Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;

  Query Match             1.2%;  Score 20;  DB 9;  Length 226475;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        429 TGGTATAGAAGCAAATGCAA 448
              ||||||||||||||||||||
Db      95864 TGGTATAGAAGCAAATGCAA 95883


RESULT 10
AAA42733/c
ID   AAA42733 standard; cDNA; 407 BP.
XX
AC   AAA42733;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human secreted expressed sequence tag SEQ ID NO:1473.
XX
KW   Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
KW   expressed sequence tag; EST; probe; chemotactic; proliferative;
KW   immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
KW   thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
KW   antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
KW   antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW   cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
KW   autoimmune disorder; multiple sclerosis; allergic condition;
KW   insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
KW   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW   central nervous system disorder; Alzheimer's disease; stroke;
KW   Parkinson's disease; Huntington's disease; coagulation disorder;
KW   haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
KW   infection; depression; psoriasis; ss.
XX
OS   Homo sapiens.
XX
```

PN WO200021990-A1.
XX
PD 20-APR-2000.
XX
PF 15-OCT-1999; 99WO-US024205.
XX
PR 15-OCT-1998; 98US-0104435P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M;
XX
DR WPI; 2000-317937/27.
XX
PT Isolated polynucleotides, and encoded proteins, comprising secreted
PT expressed sequence tags (sESTs), useful for treating various disorders
PT such as autoimmune, infectious, and central nervous system disorders.
XX
PS Claim 1; Page 468-469; 618pp; English.
XX
CC AAA41261 to AAA43419 represent specifically claimed secreted expressed
CC sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
CC sources. The sESTs can have a range of activities depending on the
CC tissues they were isolated from. The activities include: chemotactic;
CC proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
CC haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
CC antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer;
CC osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
CC cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
CC used for gene therapy and in vaccines. The sESTs are useful as probes for
CC the identification and isolation of full-length cDNAs and genomic DNA
CC molecules which correspond to the sESTs. Proteins encoded by the sESTs
CC are useful in assays for determining biological activity and raising
CC antibodies. They may be useful for treatment of autoimmune disorders
CC (multiple sclerosis, insulin dependent diabetes), allergic conditions
CC (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
CC osteoporosis, osteoarthritis, central nervous system disorders
CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
CC disease), tumours, bacterial, fungal or viral infections, depression and
CC psoriasis. AAA43420 to AAA43425 represent linker variants which are given
CC in the exemplification of the present invention
XX
SQ Sequence 407 BP; 131 A; 94 C; 126 G; 56 T; 0 U; 0 Other;

Query Match 1.2%; Score 19; DB 3; Length 407;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 703 CTTCTTGGTTCTGTTGAGG 721
||||||||||||||||||||
Db 398 CTTCTTGGTTCTGTTGAGG 380

RESULT 11
ABA08624/c
ID ABA08624 standard; cDNA; 453 BP.
XX
AC ABA08624;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:400.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11380.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 483; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 453 BP; 124 A; 112 C; 139 G; 78 T; 0 U; 0 Other;

Query Match 1.2%; Score 19; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        703 CTTCTTGGTTCTGTTGAGG 721
              ||||||||||||||||||
Db        187 CTTCTTGGTTCTGTTGAGG 169


RESULT 12
ADC32511/c
ID   ADC32511 standard; cDNA; 453 BP.
XX
AC   ADC32511;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human novel cDNA contig sequence, SEQ ID NO:2593.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; chromosome 3; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003029271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY,  Zhang J,  Ren F,  Xue AJ,  Zhao QA,  Wang J,  Wehrman T;
PI   Zhou P,  Ghosh M,  Wang D,  Ma Y,  Asundi V,  Wang Z,  Weng G;
PI   Haley-Vicente D,  Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC33278.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet
PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Example 2; SEQ ID NO 2593; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
CC   recombinant production of a polypeptide of the invention; an antibody
CC   against a polypeptide of the invention; a method of detecting
CC   polynucleotides or polypeptides of the invention; and methods of
CC   identifying a compound which binds to a polypeptide of the invention. The
CC   invention further discloses methods of peventing, treating or
CC   ameliorating a medical condition; kits comprising polynucleotide probes
CC   and/or monoclonal antibodies for carrying out the methods of the
CC   invention; methods for the identification of compounds that modulate the
CC   expression or activity of the polynucleotide and/or polypeptide; and 767
CC   contig sequences corresponding to the cDNA sequences of the invention
CC   (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC   -ADC33394). The nucleic acids and polypeptides of the invention are
CC   useful in diagnostics, drug screening, forensics, gene mapping, in the
CC   identification of mutations responsible for genetic disorders or other
CC   traits, for assessing biodiversity, and in producing many other types of
CC   data and products dependent on DNA and amino acid sequences. They are
CC   also used for treating diseases such as Parkinson's disease, Alzheimer's
CC   disease and other neurodegenerative diseases, anaemia, platelet
CC   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC   cancer. The nucleic acids may also be used as hybridisation probes or
CC   primers, and in the recombinant production of a protein. The polypeptides
CC   are also useful in generating antibodies, as molecular weight markers,
CC   and as food supplements. The present sequence represents a human contig
CC   sequence used in an example of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 453 BP; 124 A; 112 C; 139 G; 78 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 19;  DB 10;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 71;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        703 CTTCTTGGTTCTGTTGAGG 721
              ||||||||||||||||||
Db        187 CTTCTTGGTTCTGTTGAGG 169


RESULT 13
AAC76568/c
ID   AAC76568 standard; cDNA; 909 BP.
XX
AC   AAC76568;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF2123 polynucleotide sequence SEQ ID NO:4245.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive; ss.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
PF   31-MAR-2000; 2000WO-US008621.
XX
PR   31-MAR-1999;   99US-0127607P.
PR   02-APR-1999;   99US-0127636P.
PR   05-APR-1999;   99US-0127728P.
PR   30-MAR-2000; 2000US-00540763.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2000-602362/57.
DR   P-PSDB; AAB42359.
XX
PT   Novel nucleic acids and peptides derived from open reading frame X,
PT   useful for treating e.g. cancers, proliferative disorders,
PT   neurodegenerative disorders and cardiovascular disease.
XX
PS   Claim 5; Page 3441; 5507pp; English.
XX
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CC   AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC   which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC   sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC   antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC   anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC   cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC   dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC   antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC   sequences can be used for determining the presence of or predisposition
CC   to, or preventing or treating pathological conditions associated with an
CC   ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC   proteins in gene therapy vectors. The proteins and nucleic acids may be
CC   used to treat cancers, proliferative disorders, neurodegenerative
CC   disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC   diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC   storage, systemic lupus erythematosus, severe combined immunodeficiency
CC   (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC   disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC   cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC   enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ   Sequence 909 BP; 256 A; 236 C; 275 G; 141 T; 0 U; 1 Other;

  Query Match             1.2%;  Score 19;  DB 3;  Length 909;
  Best Local Similarity   100.0%;  Pred. No. 72;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        703 CTTCTTGGTTCTGTTGAGG 721
              ||||||||||||||||||||
Db        444 CTTCTTGGTTCTGTTGAGG 426


RESULT 14
ADC30740/c
ID   ADC30740 standard; cDNA; 1468 BP.
XX
AC   ADC30740;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human novel cDNA sequence, SEQ ID NO:822.
XX
KW   Human; diagnostic; drug screening; forensics; gene mapping;
KW   biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW   neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW   ulcers; osteoporosis; autoimmune disease; cancer;
KW   molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW   neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW   antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW   gene therapy; chromosome 3; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003029271-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030474.
XX
PR   24-SEP-2001; 2001US-0324631P.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang TY,  Zhang J,  Ren F,  Xue AJ,  Zhao QA,  Wang J,  Wehrman T;
PI   Zhou P,  Ghosh M,  Wang D,  Ma Y,  Asundi V,  Wang Z,  Weng G;
PI   Haley-Vicente D,  Drmanac RT;
XX
DR   WPI; 2003-371981/35.
DR   P-PSDB; ADC31711.
XX
PT   New polynucleotide and polypeptide useful for diagnosing, preventing or
PT   treating conditions such as neurodegenerative diseases, anemias, platelet
PT   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 822; 1185pp; English.
XX
CC   The invention relates to 971 novel human cDNA sequences (ADC29919-
CC   ADC30889)and the polypeptides they encode (ADC30890-ADC31860). The
CC   invention also relates to nucleic acid sequences over 99% identical with
CC   the novel human cDNAs. The invention additionally encompasses expression
CC   vectors and host cells comprising a nucleic acid of the invention; the
CC   recombinant production of a polypeptide of the invention; an antibody
CC   against a polypeptide of the invention; a method of detecting
CC   polynucleotides or polypeptides of the invention; and methods of
CC   identifying a compound which binds to a polypeptide of the invention. The
CC   invention further discloses methods of peventing, treating or
CC   ameliorating a medical condition; kits comprising polynucleotide probes
CC   and/or monoclonal antibodies for carrying out the methods of the
CC   invention; methods for the identification of compounds that modulate the
CC   expression or activity of the polynucleotide and/or polypeptide; and 767
CC   contig sequences corresponding to the cDNA sequences of the invention
CC   (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC   -ADC33394). The nucleic acids and polypeptides of the invention are
CC   useful in diagnostics, drug screening, forensics, gene mapping, in the
CC   identification of mutations responsible for genetic disorders or other
CC   traits, for assessing biodiversity, and in producing many other types of
CC   data and products dependent on DNA and amino acid sequences. They are
CC   also used for treating diseases such as Parkinson's disease, Alzheimer's
CC   disease and other neurodegenerative diseases, anaemia, platelet
CC   disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC   cancer. The nucleic acids may also be used as hybridisation probes or
CC   primers, and in the recombinant production of a protein. The polypeptides
CC   are also useful in generating antibodies, as molecular weight markers,
CC   and as food supplements. The present sequence represents a specifically
CC   claimed human cDNA sequence of the invention. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1468 BP; 375 A; 389 C; 396 G; 308 T; 0 U; 0 Other;

  Query Match             1.2%;  Score 19;  DB 10;  Length 1468;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        703 CTTCTTGGTTCTGTTGAGG 721
              ||||||||||||||||||||
Db        386 CTTCTTGGTTCTGTTGAGG 368


RESULT 15
ACA21590/c
ID   ACA21590 standard; DNA; 1584 BP.
XX
AC   ACA21590;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #3247.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Bacillus anthracis.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
```

PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU17720.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 9460; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1584 BP; 527 A; 307 C; 307 G; 443 T; 0 U; 0 Other;

Query Match 1.2%; Score 19; DB 8; Length 1584;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 591 TAATAATGTCTTCAGATAC 609
||||||||||||||||||||
Db 1564 TAATAATGTCTTCAGATAC 1546

Search completed: November 9, 2004, 04:47:07
Job time : 890 secs

OM nucleic - nucleic search, using sw model

Run on: November 9, 2004, 04:34:42 ; Search time 5405 Seconds
(without alignments)
11063.386 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgaattcgaaatc.....ttgataaaagtgggtattaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	410	25.0	596	1	AU237072	AU237072 AU237072
	2	65	4.0	625	8	BH944186	BH944186 obu90a02.
	3	58	3.5	546	9	CC948085	CC948085 BOIHF12TR
c	4	57	3.5	249	9	AJ589191	AJ589191 Arabidops
	5	57	3.5	703	8	BZ082259	BZ082259 lkv30d04.
c	6	47	2.9	673	8	BH974466	BH974466 odj06g04.
c	7	40	2.4	40	8	BH864615	BH864615 SALK_0963
c	8	33	2.0	70	8	BH847141	BH847141 SALK_0134
	9	32	2.0	207	8	BH746163	BH746163 qo78e11.b
	10	30	1.8	728	1	AU306500	AU306500 AU306500
c	11	29	1.8	303	8	BH548609	BH548609 BOHCO62TF
	12	28	1.7	1225	8	B11175	B11175 F14L4-Sp6 I
	13	24	1.5	632	4	BI922233	BI922233 EST542136
	14	24	1.5	704	4	BI422757	BI422757 EST533423
	15	24	1.5	788	7	CK259393	CK259393 EST705471
	16	24	1.5	946	7	CK259394	CK259394 EST705472
c	17	23	1.4	251	7	CN770731	CN770731 taf26e07.
c	18	23	1.4	382	8	BZ763393	BZ763393 SALK_1170
	19	23	1.4	560	6	CD710878	CD710878 VVA026C02
	20	23	1.4	565	5	BQ584361	BQ584361 E011859-0
	21	22	1.3	556	9	CL588639	CL588639 OB__Ba008
	22	22	1.3	651	9	CE521850	CE521850 tigr-gss-
c	23	22	1.3	690	4	BG703033	BG703033 602685844
c	24	22	1.3	912	4	BG180774	BG180774 602327188
c	25	21	1.3	493	9	CC948076	CC948076 BOIHF12TF
	26	21	1.3	502	7	CK115712	CK115712 Y014D01 P
c	27	20	1.2	191	2	AW057143	AW057143 ca01d02.y
	28	20	1.2	240	6	C70865	C70865 C70865 Yuji
c	29	20	1.2	303	2	BB495738	BB495738 BB495738
c	30	20	1.2	306	2	BF847741	BF847741 IL5-EN008
c	31	20	1.2	325	2	BB492868	BB492868 BB492868
	32	20	1.2	360	1	AV201222	AV201222 AV201222
	33	20	1.2	360	1	AV203275	AV203275 AV203275
	34	20	1.2	360	6	C67741	C67741 C67741 Yuji
	35	20	1.2	360	6	C69687	C69687 C69687 Yuji
	36	20	1.2	383	6	C70548	C70548 C70548 Yuji
	37	20	1.2	389	8	BH451075	BH451075 BOHFQ84TF
c	38	20	1.2	427	8	AQ198065	AQ198065 RPCI11-46
	39	20	1.2	428	4	BJ759121	BJ759121 BJ759121
c	40	20	1.2	431	8	AQ564754	AQ564754 HS_5361_A
c	41	20	1.2	434	1	AV914566	AV914566 AV914566
	42	20	1.2	478	7	CK581181	CK581181 IST_WI5_3
c	43	20	1.2	483	8	AQ493090	AQ493090 HS_5211_B
c	44	20	1.2	503	8	AQ195384	AQ195384 RPCI11-46
c	45	20	1.2	504	5	BU972434	BU972434 HB21K04r
	46	20	1.2	521	2	BF054499	BF054499 EST439729
c	47	20	1.2	553	4	BI468114	BI468114 EST00521
c	48	20	1.2	565	8	AQ372820	AQ372820 RPCI11-15
	49	20	1.2	570	8	BH107520	BH107520 RPCI-24-3
c	50	20	1.2	573	6	CA500577	CA500577 WHE4021_F
c	51	20	1.2	574	1	AV835512	AV835512 AV835512
	52	20	1.2	578	5	BX301173	BX301173 BX301173
	53	20	1.2	591	2	BF587570	BF587570 FM1_38_A0
	54	20	1.2	599	2	AW036854	AW036854 614019F11
c	55	20	1.2	608	2	BF338987	BF338987 602036062
c	56	20	1.2	638	5	BQ471308	BQ471308 HV02A09r
c	57	20	1.2	644	1	AV913458	AV913458 AV913458
c	58	20	1.2	665	6	CD900920	CD900920 G356.102D
	59	20	1.2	666	8	BH974706	BH974706 odj06g04.
	60	20	1.2	686	5	BQ508623	BQ508623 EST616038
c	61	20	1.2	690	4	BJ235635	BJ235635 BJ235635
	62	20	1.2	697	4	BI177423	BI177423 EST518368
c	63	20	1.2	703	9	CG449358	CG449358 OG7AB05TH
	64	20	1.2	703	9	CG450012	CG450012 OG7AB06TV
c	65	20	1.2	713	1	AJ611143	AJ611143 AJ611143
c	66	20	1.2	756	9	BX217764	BX217764 Danio rer
c	67	20	1.2	763	9	CC560623	CC560623 CH240_470
	68	20	1.2	792	4	BG600021	BG600021 EST504916
c	69	20	1.2	838	8	B12295	B12295 T20M5-Sp6 T
	70	20	1.2	849	3	AY108921	AY108921 Zea mays
c	71	20	1.2	889	9	CG955720	CG955720 MBEME38TR
	72	20	1.2	890	6	CD325432	CD325432 AGENCOURT
c	73	20	1.2	931	9	CG921778	CG921778 MBEHL31TR
	74	20	1.2	959	9	CC718562	CC718562 OGUDM33TH
	75	20	1.2	968	7	CK260764	CK260764 EST706842
	76	20	1.2	1002	8	AZ672942	AZ672942 ENTIV65TF
	77	20	1.2	1021	4	BG281245	BG281245 602401706
c	78	20	1.2	1030	9	CL052427	CL052427 CH216-75N
	79	20	1.2	1073	7	CK212372	CK212372 FGAS02424
c	80	20	1.2	2967	3	AK085217	AK085217 Mus muscu
	81	19	1.2	113	8	BZ383343	BZ383343 SALK_1324
c	82	19	1.2	189	5	BU917428	BU917428 JK04B05 S
	83	19	1.2	217	2	BB029739	BB029739 BB029739
c	84	19	1.2	225	1	AV367815	AV367815 AV367815
	85	19	1.2	229	1	AL599448	AL599448 DKFZp313N
c	86	19	1.2	259	7	CN556474	CN556474 tae37a11.
	87	19	1.2	267	1	AA638182	AA638182 vl96b04.r
	88	19	1.2	283	2	BB160755	BB160755 BB160755
	89	19	1.2	283	2	BB351789	BB351789 BB351789
	90	19	1.2	306	6	CD181201	CD181201 MS1-0030T
	91	19	1.2	309	1	AV051299	AV051299 AV051299
	92	19	1.2	309	2	BB498764	BB498764 BB498764
	93	19	1.2	310	1	AV277827	AV277827 AV277827
	94	19	1.2	311	6	CD553419	CD553419 B0359D11-
	95	19	1.2	314	6	CD554265	CD554265 B0373E11-
	96	19	1.2	318	2	BB167702	BB167702 BB167702
	97	19	1.2	318	2	BB341313	BB341313 BB341313

c 98	19	1.2	318	2	BB491357	BB491357	BB491357
99	19	1.2	325	2	BB218348	BB218348	BB218348
100	19	1.2	343	4	BJ454495	BJ454495	BJ454495
101	19	1.2	346	7	CR466415	CR466415	CR466415
102	19	1.2	360	5	BY380442	BY380442	BY380442
c 103	19	1.2	383	9	CC929527	CC929527	ZMMBBc053
c 104	19	1.2	405	1	AI115594	AI115594	uh87e04.r
105	19	1.2	415	2	BF715659	BF715659	mab10b09.
c 106	19	1.2	426	7	H56980	H56980	yr07a03.r1
c 107	19	1.2	429	1	AU267362	AU267362	AU267362
108	19	1.2	434	2	BB750671	BB750671	BB750671
109	19	1.2	436	7	CK096173	CK096173	UA50BPC12
110	19	1.2	439	2	AW053755	AW053755	L30-1648T
111	19	1.2	440	1	AA896937	AA896937	L30-369T3
c 112	19	1.2	443	8	AZ259430	AZ259430	RPCI-23-1
113	19	1.2	466	7	CN465987	CN465987	LcB002D16
114	19	1.2	468	1	AA856218	AA856218	L30-239T3
c 115	19	1.2	471	8	AZ163210	AZ163210	SP_0073_A
c 116	19	1.2	472	5	BU820015	BU820015	UA50BPC12
c 117	19	1.2	475	8	BZ120282	BZ120282	CH230-264
118	19	1.2	476	1	AA734960	AA734960	vs78d08.r
119	19	1.2	476	1	AA154747	AA154747	mt64e03.r
120	19	1.2	476	9	AG227482	AG227482	Lotus cor
121	19	1.2	482	8	BH004158	BH004158	BMBAC07I0
c 122	19	1.2	486	8	BH184362	BH184362	025_G_12-
c 123	19	1.2	486	9	CNS07PBK	AL621314	T3 end of
124	19	1.2	509	4	BJ454333	BJ454333	BJ454333
c 125	19	1.2	510	6	CB487034	CB487034	omykrtdh0
126	19	1.2	513	6	CA990677	CA990677	EST644185
127	19	1.2	515	5	BU761169	BU761169	sas64a12.
c 128	19	1.2	517	7	CK106007	CK106007	UA50BPC12
c 129	19	1.2	520	6	CA355869	CA355869	627850 NC
130	19	1.2	521	8	AQ835756	AQ835756	HS_4674_A
c 131	19	1.2	529	2	BB855462	BB855462	BB855462
132	19	1.2	529	5	BX524700	BX524700	BX524700
c 133	19	1.2	537	1	AI505267	AI505267	vp97f12.x
c 134	19	1.2	537	9	CC902352	CC902352	ZMMBBb024
c 135	19	1.2	543	2	AW935968	AW935968	QV3-DT001
136	19	1.2	543	6	CF164602	CF164602	B0745C03-
137	19	1.2	550	4	BG088851	BG088851	H3158D07-
c 138	19	1.2	553	2	BE853020	BE853020	uw28d11.x
139	19	1.2	553	4	BG246682	BG246682	602360740
140	19	1.2	558	2	BE116922	BE116922	UI-R-BS1-
141	19	1.2	568	4	BI774098	BI774098	466076 MA
142	19	1.2	573	8	AZ232370	AZ232370	RPCI-23-6
143	19	1.2	581	2	AW973353	AW973353	EST385496
144	19	1.2	584	6	CA340901	CA340901	haa73c02.
145	19	1.2	584	6	CF163855	CF163855	B0734A05-
146	19	1.2	604	9	CR315959	CR315959	Medicago
c 147	19	1.2	609	5	BQ826913	BQ826913	gd49a11.x
148	19	1.2	609	7	CF917504	CF917504	Bflor498.
149	19	1.2	611	4	BI383705	BI383705	BFLG2_001
150	19	1.2	614	1	AV909896	AV909896	AV909896
c 151	19	1.2	617	5	BU814993	BU814993	N035H03 P
c 152	19	1.2	619	1	AL596750	AL596750	DKFZp451D
153	19	1.2	619	2	BF024794	BF024794	dd11d10.y
154	19	1.2	623	8	BZ271453	BZ271453	CH230-410
155	19	1.2	630	6	CD770392	CD770392	AGENCOURT
c 156	19	1.2	631	6	CB246853	CB246853	UI-M-FI0-
157	19	1.2	631	6	CD771359	CD771359	AGENCOURT
c 158	19	1.2	634	9	CE615147	CE615147	tigr-gss-
c 159	19	1.2	636	6	CF232420	CF232420	PtaJXO001
160	19	1.2	637	8	AQ814411	AQ814411	HS_5511_B
c 161	19	1.2	639	6	CA380888	CA380888	660286 NC
c 162	19	1.2	643	5	BQ584761	BQ584761	E013262-0
c 163	19	1.2	647	5	BU832766	BU832766	T038A04 P
c 164	19	1.2	648	6	BY726789	BY726789	BY726789
165	19	1.2	655	9	CR485220	CR485220	Medicago
166	19	1.2	658	6	CB551588	CB551588	MMSP0033_
167	19	1.2	659	9	BX123534	BX123534	Danio rer
c 168	19	1.2	661	5	BU893991	BU893991	P085F02 P
c 169	19	1.2	662	5	BU251577	BU251577	603402768
170	19	1.2	674	2	BB207669	BB207669	BB207669
c 171	19	1.2	674	9	CE425314	CE425314	CE425314
172	19	1.2	675	4	BG449977	BG449977	BG449977
173	19	1.2	676	8	AZ789485	AZ789485	AZ789485
c 174	19	1.2	677	4	BI309412	BI309412	EST530822
175	19	1.2	678	2	BB200448	BB200448	BB200448
176	19	1.2	681	6	CB488869	CB488869	omykrtah0
177	19	1.2	689	1	AI065163	AI065163	HA1005 Hu
178	19	1.2	699	5	BQ863393	BQ863393	QGC23M06.
179	19	1.2	699	5	BX310965	BX310965	BX310965
c 180	19	1.2	701	5	BU871322	BU871322	Q029C09 P
181	19	1.2	702	8	BZ105069	BZ105069	CH230-227
c 182	19	1.2	702	9	CC786947	CC786947	ZMMBBb015
183	19	1.2	703	9	CE552010	CE552010	tigr-gss-
c 184	19	1.2	712	9	AG329124	AG329124	Mus muscu
185	19	1.2	723	9	AG393024	AG393024	Mus muscu
186	19	1.2	724	8	BH422051	BH422051	BOHNP05TR
187	19	1.2	726	4	BG921389	BG921389	602824256
188	19	1.2	733	9	CG682692	CG682692	ZMMBBc015
189	19	1.2	743	7	CK636205	CK636205	UI-M-HN0-
190	19	1.2	752	2	BE916493	BE916493	601667068
191	19	1.2	754	4	BI558629	BI558629	603240636
192	19	1.2	756	8	AQ919963	AQ919963	RPCI-23-2
193	19	1.2	758	9	AG540973	AG540973	Mus muscu
194	19	1.2	761	8	BH456377	BH456377	BOGVO58TR
c 195	19	1.2	763	7	CO046417	CO046417	UI-M-HU0-
196	19	1.2	764	9	CL400513	CL400513	ZMMBBb039
c 197	19	1.2	769	8	BZ077376	BZ077376	lky31c03.
c 198	19	1.2	780	7	CN053715	CN053715	Salamande
c 199	19	1.2	784	5	BU283961	BU283961	603862865
200	19	1.2	798	4	BG584891	BG584891	EST486652
c 201	19	1.2	806	9	CG675565	CG675565	trs3297 t
202	19	1.2	808	8	BZ435706	BZ435706	BONNU12TF
c 203	19	1.2	813	6	CA922278	CA922278	EST639996
204	19	1.2	817	9	CG919282	CG919282	MBEAT07TR
205	19	1.2	820	5	BX927594	BX927594	BX927594
206	19	1.2	821	9	CL140900	CL140900	ISB1-118B
207	19	1.2	822	6	CA846248	CA846248	haa11d09.
208	19	1.2	837	2	BE642769	BE642769	Cri2_6_P0
c 209	19	1.2	843	2	BF623020	BF623020	HVSMEa001
210	19	1.2	856	4	BI659584	BI659584	603303137
211	19	1.2	875	9	CG919226	CG919226	MBEBH26TF
212	19	1.2	878	5	BQ733857	BQ733857	AGENCOURT
c 213	19	1.2	891	5	BQ433760	BQ433760	AGENCOURT
c 214	19	1.2	893	1	AA203733	AA203733	zx53h04.r
c 215	19	1.2	903	8	CC125140	CC125140	NDL.78J23
c 216	19	1.2	912	9	CC875163	CC875163	HSC 00701
217	19	1.2	915	5	BQ135466	BQ135466	NF006F07E
218	19	1.2	916	8	CC143740	CC143740	NDL.18L12
219	19	1.2	920	2	BE794531	BE794531	601590285
220	19	1.2	932	7	CN645048	CN645048	ILLUMIGEN
221	19	1.2	935	2	BB614286	BB614286	BB614286
c 222	19	1.2	936	3	CNS0A340	BX828364	Arabidops
223	19	1.2	945	8	CC223500	CC223500	CH261-105
224	19	1.2	950	2	BF180992	BF180992	601805038
225	19	1.2	964	9	CNS02V08	AL215153	Tetraodon
226	19	1.2	972	6	BY711192	BY711192	BY711192
c 227	19	1.2	972	9	CL471665	CL471665	SAIL_164_
228	19	1.2	990	5	BU504817	BU504817	AGENCOURT
c 229	19	1.2	994	2	BE613522	BE613522	601504278
230	19	1.2	1021	9	CL114127	CL114127	ISB1-59K2
231	19	1.2	1052	3	AK029452	AK029452	Mus muscu
232	19	1.2	1111	3	AK040295	AK040295	Mus muscu
c 233	19	1.2	1113	8	BZ562981	BZ562981	pacs2-164
c 234	19	1.2	1190	8	BZ578287	BZ578287	msh2_5773
235	19	1.2	1238	8	BH770371	BH770371	LLMGtag14
236	19	1.2	1344	2	BF577525	BF577525	602092378
237	19	1.2	1525	3	AK011996	AK011996	Mus muscu
238	19	1.2	3543	3	AK079056	AK079056	Mus muscu
239	18	1.1	180	1	AA783081	AA783081	a5d09a1.f
c 240	18	1.1	216	8	AZ889109	AZ889109	RPCI-24-1
c 241	18	1.1	218	2	BE159187	BE159187	MR0-HT040
c 242	18	1.1	220	1	AA169312	AA169312	zp20e06.r
c 243	18	1.1	221	6	CD492298	CD492298	DD6-87E D

c	244	18	1.1	221	7	CR581072	CR581072 CR581072	c	317	18	1.1	396	7	CK579958	CK579958 IST_WI5_2
	245	18	1.1	223	9	CG710218	CG710218 1119016E0		318	18	1.1	397	2	BF013824	BF013824 ro12f07.y
c	246	18	1.1	224	8	AQ531687	AQ531687 RPCI-11-3	c	319	18	1.1	397	9	CC602321	CC602321 ZMMBBc041
c	247	18	1.1	227	7	CR581074	CR581074 CR581074		320	18	1.1	398	6	BY691704	BY691704 BY691704
	248	18	1.1	231	9	CG786555	CG786555 ZMMBBb013	c	321	18	1.1	399	9	CC929962	CC929962 ZMMBBc053
	249	18	1.1	238	9	CL239137	CL239137 ZMMBBb058		322	18	1.1	403	2	BE820954	BE820954 GM700013B
	250	18	1.1	239	1	AI151937	AI151937 ui48a01.y		323	18	1.1	404	8	BZ708056	BZ708056 OGBAP12TC
c	251	18	1.1	239	1	AA410532	AA410532 zv23a04.r	c	324	18	1.1	405	2	AW733457	AW733457 sk73g12.y
c	252	18	1.1	241	4	BM151497	BM151497 TCBAP1D92		325	18	1.1	406	1	AA785018	AA785018 g4c08a1.f
	253	18	1.1	249	9	CE390107	CE390107 tigr-gss-		326	18	1.1	409	4	BG662434	BG662434 Ljirnpest
c	254	18	1.1	255	4	BI403556	BI403556 MI-P-CP1-	c	327	18	1.1	411	2	BE024012	BE024012 sm95d06.y
	255	18	1.1	258	1	AI867614	AI867614 wb76d07.x	c	328	18	1.1	414	4	BG614684	BG614684 602642178
	256	18	1.1	260	7	CR581075	CR581075 CR581075		329	18	1.1	414	8	AQ106506	AQ106506 HS_3088_B
	257	18	1.1	261	7	CR581073	CR581073 CR581073		330	18	1.1	415	2	BF595358	BF595358 su65c03.y
	258	18	1.1	262	1	AA303749	AA303749 EST16432	c	331	18	1.1	416	1	AU284193	AU284193 AU284193
	259	18	1.1	265	2	BB565597	BB565597 BB565597		332	18	1.1	416	5	BX279797	BX279797 BX279797
c	260	18	1.1	265	9	CC854847	CC854847 NDL.64I10	c	333	18	1.1	418	4	BG882817	BG882817 sae52h10.
c	261	18	1.1	268	2	AW783719	AW783719 rp01h08.y	c	334	18	1.1	418	9	CL003739	CL003739 gbs1_VM5_
	262	18	1.1	272	7	CK987737	CK987737 SP10-D4(P	c	335	18	1.1	422	2	AW457854	AW457854 sh88b08.y
c	263	18	1.1	284	2	BB741048	BB741048 BB741048	c	336	18	1.1	425	6	CD178945	CD178945 MS1-0014P
c	264	18	1.1	284	4	BI177887	BI177887 EST518832	c	337	18	1.1	428	2	AW504350	AW504350 UI-HF-BN0
	265	18	1.1	287	2	BB331214	BB331214 BB331214		338	18	1.1	428	6	CB094320	CB094320 hx18e03.b
c	266	18	1.1	293	8	AQ684988	AQ684988 HS_5488_B		339	18	1.1	428	7	N40274	N40274 yx80a05.r1
c	267	18	1.1	294	8	AZ909584	AZ909584 RPCI-24-8	c	340	18	1.1	431	4	BI815066	BI815066 PfESToaa1
c	268	18	1.1	295	2	AW856166	AW856166 RC1-CT028		341	18	1.1	431	4	BM689921	BM689921 UI-E-CK1-
	269	18	1.1	301	7	T35234	T35234 EST81805 Hu	c	342	18	1.1	432	9	CE761730	CE761730 tigr-gss-
	270	18	1.1	301	7	W12301	W12301 ma57a05.r1		343	18	1.1	433	2	BF566310	BF566310 UI-R-BT1-
c	271	18	1.1	304	8	BZ708067	BZ708067 OGBAP12TM		344	18	1.1	434	2	AW028752	AW028752 wv34e07.x
c	272	18	1.1	306	1	AJ670617	AJ670617 AJ670617		345	18	1.1	434	5	BQ863085	BQ863085 QGC22023.
	273	18	1.1	311	1	AV827958	AV827958 AV827958		346	18	1.1	436	1	AJ648090	AJ648090 AJ648090
c	274	18	1.1	316	2	BB271409	BB271409 BB271409	c	347	18	1.1	437	6	CD992551	CD992551 QBA1h06.y
c	275	18	1.1	318	4	BI022005	BI022005 CM3-MT029		348	18	1.1	437	7	R35440	R35440 yh80a08.r1
c	276	18	1.1	318	6	CD073704	CD073704 MA3-0001U		349	18	1.1	438	4	BM857145	BM857145 K-EST0141
c	277	18	1.1	319	9	CG824214	CG824214 SOYAV77TH		350	18	1.1	438	5	BQ694412	BQ694412 1000555 H
	278	18	1.1	324	1	AJ497021	AJ497021 AJ497021	c	351	18	1.1	439	1	AJ655627	AJ655627 AJ655627
c	279	18	1.1	324	4	BI022010	BI022010 CM3-MT029		352	18	1.1	439	2	BE813533	BE813533 RC1-BN003
c	280	18	1.1	324	7	CK766729	CK766729 ltu01-7ms		353	18	1.1	439	8	AQ773481	AQ773481 HS_2212_B
c	281	18	1.1	332	2	BF814934	BF814934 IL5-CI014	c	354	18	1.1	440	7	H46292	H46292 yo19d04.s1
c	282	18	1.1	336	1	AV772113	AV772113 AV772113		355	18	1.1	441	1	AA930440	AA930440 vs58h08.r
	283	18	1.1	337	7	Z24989	Z24989 HSB81C062 S	c	356	18	1.1	442	9	CE541720	CE541720 tigr-gss-
c	284	18	1.1	340	8	AQ102443	AQ102443 HS_3038_B	c	357	18	1.1	443	6	CD158541	CD158541 ML1-0059T
c	285	18	1.1	341	7	N97698	N97698 1130C3 czap		358	18	1.1	446	9	TA125D07P	AL463186 T. brucei
c	286	18	1.1	344	4	BJ215679	BJ215679 BJ215679	c	359	18	1.1	447	1	AJ791935	AJ791935 AJ791935
c	287	18	1.1	345	2	AW383522	AW383522 PM1-HT035		360	18	1.1	447	6	CB746984	CB746984 AMGNNUC:S
	288	18	1.1	345	6	BY774937	BY774937.BY774937		361	18	1.1	447	7	CR547315	CR547315 DKFZp468K
	289	18	1.1	347	1	AV696774	AV696774 AV696774		362	18	1.1	447	8	AQ704740	AQ704740 HS_5517_A
	290	18	1.1	347	8	BZ107941	BZ107941 CH230-230		363	18	1.1	448	2	AW829068	AW829068 ra33g04.y
c	291	18	1.1	347	9	CC811523	CC811523 ZMMBBc047	c	364	18	1.1	449	6	CD178585	CD178585 MS1-0014P
	292	18	1.1	348	1	AI213899	AI213899 z7a06a1.f		365	18	1.1	453	7	W95309	W95309 ze05f08.r1
	293	18	1.1	348	7	T34563	T34563 EST70629 Hu		366	18	1.1	454	8	AQ674105	AQ674105 HS_5483_B
c	294	18	1.1	349	5	BQ510059	BQ510059 EST617474	c	367	18	1.1	456	2	BF423682	BF423682 sr38d10.y
	295	18	1.1	359	4	BJ465223	BJ465223 BJ465223	c	368	18	1.1	457	8	AQ056241	AQ056241 CIT-HSP-2
c	296	18	1.1	359	6	CD144258	CD144258 MG1-0094T		369	18	1.1	460	2	BE028794	BE028794 EtESTea84
c	297	18	1.1	360	8	B38290	B38290 HS-1047-A2-		370	18	1.1	461	4	BI432500	BI432500 EST535261
	298	18	1.1	363	2	BE081644	BE081644 QV2-BT063	c	371	18	1.1	461	4	BM404578	BM404578 EST578905
	299	18	1.1	365	6	CA002004	CA002004 HS06D19r		372	18	1.1	461	6	CB737224	CB737224 AMGNNUC:M
c	300	18	1.1	367	4	BI678512	BI678512 SWS286 SW	c	373	18	1.1	462	4	BI403472	BI403472 MI-P-CP1-
	301	18	1.1	368	9	CE839709	CE839709 tigr-gss-		374	18	1.1	462	6	CB159560	CB159560 K-EST0219
	302	18	1.1	370	8	AQ261286	AQ261286 CITBI-E1-	c	375	18	1.1	463	6	C22476	C22476 C22476 Rice
c	303	18	1.1	371	6	CD190591	CD190591 MS1-0064U	c	376	18	1.1	465	4	BI538390	BI538390 428952 MA
	304	18	1.1	371	9	CG701469	CG701469 ZMMBBc017	c	377	18	1.1	466	1	AA455642	AA455642 aa22c02.s
c	305	18	1.1	374	8	AZ910802	AZ910802 RPCI-24-1	c	378	18	1.1	467	6	C22475	C22475 C22475 Rice
c	306	18	1.1	375	5	BY583614	BY583614 BY583614		379	18	1.1	470	2	BE120939	BE120939 UI-R-CA0-
	307	18	1.1	375	7	Z18066	Z18066 ATTS0552 Ve		380	18	1.1	471	6	CB732706	CB732706 AMGNNUC:C
	308	18	1.1	382	7	T10644	T10644 hbc774 Huma		381	18	1.1	473	9	CG218941	CG218941 OGXEB37TH
c	309	18	1.1	386	4	BM698701	BM698701 UI-E-DX1-		382	18	1.1	474	8	BZ371230	BZ371230 ie32f02.b
	310	18	1.1	388	1	AA218702	AA218702 zq96h09.r		383	18	1.1	475	2	BF977614	BF977614 602147406
c	311	18	1.1	389	9	CC794687	CC794687 SALK_0540	c	384	18	1.1	477	1	AI607134	AI607134 ms22g02.y
c	312	18	1.1	391	5	BU894286	BU894286 X005G04 P	c	385	18	1.1	477	1	AA168119	AA168119 ms22g02.r
	313	18	1.1	391	9	CG710221	CG710221 1119016E0		386	18	1.1	478	5	BQ506820	BQ506820 EST614235
	314	18	1.1	392	1	AV426830	AV426830 AV426830	c	387	18	1.1	479	4	BG596474	BG596474 EST495152
	315	18	1.1	395	1	AL789130	AL789130 AL789130	c	388	18	1.1	479	8	CC161969	CC161969 ii80g08.g
	316	18	1.1	395	9	CG398021	CG398021 ZMMBBc002		389	18	1.1	480	8	BH754545	BH754545 SALK_0425

c	390	18	1.1	480	8	CC167990	CC167990 ij78g08.g	c	463	18	1.1	553	4	BJ429228	BJ429228	BJ429228
c	391	18	1.1	481	1	AJ684236	AJ684236 AJ684236	c	464	18	1.1	553	4	BM404728	BM404728	EST579055
	392	18	1.1	481	2	AW828867	AW828867 ra69b05.y		465	18	1.1	554	1	AA595248	AA595248	no33b06.s
c	393	18	1.1	481	4	BG652739	BG652739 sad71d02.		466	18	1.1	554	8	BH426893	BH426893	BOHKF40TF
c	394	18	1.1	481	8	BH254577	BH254577 SALK_0167		467	18	1.1	556	5	BX345548	BX345548	BX345548
	395	18	1.1	483	1	AI568433	AI568433 tn39c02.x		468	18	1.1	557	9	CE391411	CE391411	tigr-gss-
c	396	18	1.1	488	1	AI151986	AI151986 ud18b06.r	c	469	18	1.1	558	4	BJ003446	BJ003446	BJ003446
	397	18	1.1	489	7	CN783426	CN783426 ai_3000.0		470	18	1.1	559	6	CB160944	CB160944	K-EST0220
c	398	18	1.1	489	9	CL804482	CL804482 OR_CBa001	c	471	18	1.1	559	8	AQ283347	AQ283347	RPCI11-91
c	399	18	1.1	491	4	BG589518	BG589518 EST497360	c	472	18	1.1	560	4	BI425875	BI425875	sah73d09.
c	400	18	1.1	491	4	BM109645	BM109645 EST557181	c	473	18	1.1	560	5	BM955054	BM955054	sam76d07.
c	401	18	1.1	491	6	CA263060	CA263060 SCPRLB202	c	474	18	1.1	560	7	CO103474	CO103474	GR__Eb003
c	402	18	1.1	491	7	CF503811	CF503811 USDA-FP_1		475	18	1.1	561	4	BJ187743	BJ187743	BJ187743
	403	18	1.1	492	6	CB145272	CB145272 K-EST0200		476	18	1.1	561	6	CD115621	CD115621	ME1-0038P
c	404	18	1.1	494	2	AW248840	AW248840 2820786.3	c	477	18	1.1	562	8	BZ934379	BZ934379	CH240_90O
c	405	18	1.1	495	9	BX982305	BX982305 Forward s		478	18	1.1	563	6	CB547824	CB547824	AMGNNUC:N
	406	18	1.1	497	6	CB074145	CB074145 EST01776	c	479	18	1.1	567	5	BP137222	BP137222	BP137222
	407	18	1.1	497	9	AG263970	AG263970 Lotus cor	c	480	18	1.1	568	9	CL682244	CL682244	PRI0133b_
	408	18	1.1	498	6	CD925754	CD925754 G750.118I	c	481	18	1.1	569	6	CA380776	CA380776	660143 NC
c	409	18	1.1	500	5	BQ506819	BQ506819 EST614234		482	18	1.1	569	6	CB075182	CB075182	hz40d07.b
	410	18	1.1	500	8	CC161968	CC161968 ii80g08.b	c	483	18	1.1	570	4	BM127434	BM127434	ie95c08.y
c	411	18	1.1	501	8	BZ924112	BZ924112 CH240_117		484	18	1.1	570	5	BQ865763	BQ865763	QGC5N01.y
	412	18	1.1	501	8	CC167989	CC167989 ij78g08.b	c	485	18	1.1	570	9	CE485710	CE485710	tigr-gss-
c	413	18	1.1	503	8	AZ466516	AZ466516 1M0277H15	c	486	18	1.1	570	9	CG817791	CG817791	SOYAU07TH
	414	18	1.1	503	9	AG251862	AG251862 Lotus cor		487	18	1.1	571	5	BX517265	BX517265	BX517265
	415	18	1.1	504	4	BG551652	BG551652 sad41b05.		488	18	1.1	571	8	BZ327456	BZ327456	id27d03.g
	416	18	1.1	506	6	CA409880	CA409880 1438_F -P	c	489	18	1.1	572	9	CC766779	CC766779	CH240_132
c	417	18	1.1	507	1	AA393880	AA393880 zv64a01.r		490	18	1.1	574	6	CD735745	CD735745	4016653 1
c	418	18	1.1	507	8	AQ814554	AQ814554 HS_5265_A		491	18	1.1	574	6	CF212579	CF212579	CGF100065
c	419	18	1.1	508	1	AI153147	AI153147 ud55c09.r	c	492	18	1.1	575	4	BI917449	BI917449	603185107
	420	18	1.1	508	9	AG260079	AG260079 Lotus cor		493	18	1.1	576	2	BE617393	BE617393	601442028
c	421	18	1.1	510	1	AA461142	AA461142 zx64g04.r	c	494	18	1.1	576	7	CK717369	CK717369	17200 Swo
	422	18	1.1	510	5	BW192142	BW192142 BW192142		495	18	1.1	577	7	CO237275	CO237275	WS0072.B2
c	423	18	1.1	512	5	BX505303	BX505303 DKFZp686I	c	496	18	1.1	578	7	CK591230	CK591230	est_1_van
	424	18	1.1	514	8	AZ105134	AZ105134 RPCI-23-4		497	18	1.1	580	4	BG522725	BG522725	24-77 Ste
c	425	18	1.1	520	8	BH780007	BH780007 fzmb014f0		498	18	1.1	580	7	CN294457	CN294457	170005322
c	426	18	1.1	521	9	BX962792	BX962792 Forward s		499	18	1.1	582	2	BF713496	BF713496	MI-P-O3-a
	427	18	1.1	522	8	AQ185183	AQ185183 HS_2229_B		500	18	1.1	583	5	BQ862987	BQ862987	QGC22K16.
	428	18	1.1	523	1	AL959166	AL959166 AL959166	c	501	18	1.1	585	8	AQ354312	AQ354312	CITBI-E1-
c	429	18	1.1	526	6	CD178416	CD178416 MS1-0014P	c	502	18	1.1	586	2	AW629029	AW629029	hi46g12.x
	430	18	1.1	528	1	AI497317	AI497317 fb64a06.y		503	18	1.1	586	8	BZ910263	BZ910263	CH240_101
c	431	18	1.1	528	8	AQ788581	AQ788581 HS_5453_B		504	18	1.1	589	9	CE656098	CE656098	tigr-gss-
	432	18	1.1	528	8	BH787092	BH787092 fzmb014f0		505	18	1.1	590	1	AA306143	AA306143	EST177121
c	433	18	1.1	531	7	H71261	H71261 yu54b02.r1		506	18	1.1	590	4	BM729099	BM729099	UI-E-EO1-
	434	18	1.1	532	5	BX784355	BX784355 BX784355		507	18	1.1	590	6	CA639029	CA639029	wre1n.pk0
	435	18	1.1	532	8	CC462246	CC462246 ZMMBBc035	c	508	18	1.1	594	1	AA099001	AA099001	zn45e02.s
c	436	18	1.1	533	2	AW451811	AW451811 UI-H-BI3-	c	509	18	1.1	594	1	AI659165	AI659165	tu02b02.x
c	437	18	1.1	533	8	AQ611524	AQ611524 HS_5084_B	c	510	18	1.1	594	2	AW970501	AW970501	EST382582
	438	18	1.1	536	1	AA149792	AA149792 zo01c08.r	c	511	18	1.1	594	6	CB382425	CB382425	TgESTzyg7
	439	18	1.1	536	4	BG145126	BG145126 ut76a05.y	c	512	18	1.1	594	7	CK906074	CK906074	ie95c08.y
	440	18	1.1	537	2	BE780352	BE780352 601468455		513	18	1.1	595	2	BE169770	BE169770	PM1-HT052
	441	18	1.1	538	7	N32683	N32683 yx77h11.r1	c	514	18	1.1	595	6	CB165610	CB165610	BEQ603161
	442	18	1.1	538	9	CE197621	CE197621 tigr-gss-	c	515	18	1.1	595	6	CF212478	CF212478	CGF100065
	443	18	1.1	540	2	BE080214	BE080214 RC4-BT062	c	516	18	1.1	596	9	CG789522	CG789522	ZMMBBb026
	444	18	1.1	540	5	BU416371	BU416371 603671459		517	18	1.1	598	4	BG083553	BG083553	H3088F07-
c	445	18	1.1	541	4	BM085712	BM085712 saj28e04.		518	18	1.1	599	2	BE189573	BE189573	db67d10.x
	446	18	1.1	542	1	AA486489	AA486489 ab38e03.r		519	18	1.1	599	5	BQ999139	BQ999139	QGG21D19.
	447	18	1.1	542	2	BE169688	BE169688 PM1-HT052	c	520	18	1.1	600	6	CB368080	CB368080	TgESTzyg3
	448	18	1.1	543	4	BI536203	BI536203 390685 MA		521	18	1.1	600	7	CN180853	CN180853	dba05h03.
c	449	18	1.1	544	4	BG595004	BG595004 EST493682		522	18	1.1	601	4	BG260149	BG260149	602371246
c	450	18	1.1	544	4	BM113404	BM113404 EST560940		523	18	1.1	602	2	BE075337	BE075337	PM0-BT058
	451	18	1.1	544	5	BU416930	BU416930 603671445		524	18	1.1	602	7	CK541537	CK541537	rswhb0_00
c	452	18	1.1	544	6	CD051535	CD051535 ds183 P.		525	18	1.1	602	8	BH787410	BH787410	fzmb014f0
	453	18	1.1	544	8	AQ623717	AQ623717 HS_5319_A	c	526	18	1.1	603	1	AL602675	AL602675	DKFZp686P
	454	18	1.1	545	7	CK558969	CK558969 rswpb0_00	c	527	18	1.1	603	2	BE536326	BE536326	601062524
c	455	18	1.1	545	8	AQ375994	AQ375994 RPCI11-16		528	18	1.1	603	9	CR322093	CR322093	Medicago
c	456	18	1.1	546	7	W58438	W58438 zd25e05.s1	c	529	18	1.1	604	6	CD702640	CD702640	EST19165
	457	18	1.1	547	1	AJ516844	AJ516844 AJ516844		530	18	1.1	607	4	BJ027516	BJ027516	BJ027516
c	458	18	1.1	547	8	AQ969492	AQ969492 LERJN59TR		531	18	1.1	607	4	BJ214359	BJ214359	BJ214359
c	459	18	1.1	548	2	AW992977	AW992977 RC2-BN003	c	532	18	1.1	607	8	BZ531340	BZ531340	OGADV85TC
	460	18	1.1	549	7	CK744483	CK744483 nad03-13c	c	533	18	1.1	608	6	CB639379	CB639379	OSJNEa10F
	461	18	1.1	549	7	CK756189	CK756189 nad03-9cs		534	18	1.1	608	8	AZ526729	AZ526729	259PbA06
c	462	18	1.1	550	7	CN357794	CN357794 170006001	c	535	18	1.1	609	6	CB478013	CB478013	jns29_A04

	536	18	1.1	610	7	CR448952	CR448952 CR448952
	537	18	1.1	611	1	AL036362	AL036362 DKFZp564C
	538	18	1.1	611	9	AG259200	AG259200 Lotus cor
	539	18	1.1	612	6	CB922780	CB922780 VVD087H04
	540	18	1.1	612	8	AQ238696	AQ238696 RPCI11-64
	541	18	1.1	613	9	DR22P24S	AL734221 Danio rer
	542	18	1.1	613	9	CC698850	CC698850 OGUCN43TH
c	543	18	1.1	614	4	BM726216	BM726216 UI-E-EJ0-
	544	18	1.1	615	4	BG938912	BG938912 cn29b07.x
c	545	18	1.1	615	6	CB154400	CB154400 K-EST0212
c	546	18	1.1	617	4	BG498295	BG498295 602543762
c	547	18	1.1	618	6	CD051653	CD051653 ds310 P.
c	548	18	1.1	618	8	AZ863137	AZ863137 2M0171F10
	549	18	1.1	619	7	CN825354	CN825354 LjPEST5g0
c	550	18	1.1	619	8	BH869021	BH869021 hl41e04.g
	551	18	1.1	620	4	BI861281	BI861281 603391072
	552	18	1.1	620	8	AQ969653	AQ969653 LERJP12TF
c	553	18	1.1	621	8	BZ777573	BZ777573 iil1d05.g
c	554	18	1.1	622	8	BH727789	BH727789 BOMEN23TF
c	555	18	1.1	622	8	CC164253	CC164253 ii84b11.g
	556	18	1.1	622	9	CE241006	CE241006 tigr-gss-
	557	18	1.1	624	4	BJ287079	BJ287079 BJ287079
c	558	18	1.1	626	2	BB192694	BB192694 BB192694
	559	18	1.1	629	2	AW961701	AW961701 EST373774
c	560	18	1.1	629	9	CL747363	CL747363 OR_BBa011
c	561	18	1.1	630	4	BM104136	BM104136 fv47d12.x
c	562	18	1.1	631	1	AA138702	AA138702 mq40c12.r
c	563	18	1.1	631	9	CR506463	CR506463 Medicago
c	564	18	1.1	631	9	CL785973	CL785973 OR_BBa010
	565	18	1.1	632	5	BQ869775	BQ869775 QGD7C22.y
	566	18	1.1	632	5	BU370556	BU370556 603598638
c	567	18	1.1	632	6	CB133822	CB133822 K-EST0185
	568	18	1.1	634	5	BU487139	BU487139 604125840
	569	18	1.1	634	6	CA731063	CA731063 wip1c.pk0
	570	18	1.1	634	8	BH815350	BH815350 AM__Ba001
c	571	18	1.1	634	9	CE110133	CE110133 tigr-gss-
	572	18	1.1	636	2	BE080127	BE080127 RC4-BT062
	573	18	1.1	637	6	CF249426	CF249426 it73c05.y
c	574	18	1.1	639	4	BJ492266	BJ492266 BJ492266
	575	18	1.1	639	6	CD675979	CD675979 fs30f03.y
	576	18	1.1	640	2	AW992991	AW992991 RC2-BN003
c	577	18	1.1	640	5	BQ160379	BQ160379 WHE1808_C
c	578	18	1.1	641	9	CE561789	CE561789 tigr-gss-
c	579	18	1.1	644	8	BZ906825	BZ906825 CH240_30I
c	580	18	1.1	644	9	CC957667	CC957667 BOIBBI3TF
	581	18	1.1	645	5	BU416433	BU416433 603671538
c	582	18	1.1	645	6	CA132978	CA132978 SCEQRT102
c	583	18	1.1	645	7	CN263925	CN263925 170005328
	584	18	1.1	645	8	BH705334	BH705334 BOMCK44TF
c	585	18	1.1	645	9	CE126125	CE126125 tigr-gss-
c	586	18	1.1	646	8	AZ721799	AZ721799 RPCI-24-1
c	587	18	1.1	647	4	BG694768	BG694768 NISC_iv07
c	588	18	1.1	647	7	CN263929	CN263929 170005318
	589	18	1.1	648	7	CK500814	CK500814 rswbb0_01
	590	18	1.1	648	9	CG817343	CG817343 SOYER10TV
	591	18	1.1	649	5	BU416388	BU416388 603670560
	592	18	1.1	650	5	BP182737	BP182737 BP182737
c	593	18	1.1	650	9	BX148733	BX148733 Danio rer
	594	18	1.1	651	6	CD207749	CD207749 HS1_34_E0
c	595	18	1.1	651	8	AZ251708	AZ251708 RPCI-23-7
c	596	18	1.1	651	8	AZ440503	AZ440503 1M0231P06
	597	18	1.1	652	4	BI919186	BI919186 603177996
	598	18	1.1	652	8	CC324103	CC324103 TAM32-22G
c	599	18	1.1	653	1	AI122253	AI122253 uc60d07.r
c	600	18	1.1	653	5	BU357931	BU357931 603478547
c	601	18	1.1	653	6	CF135748	CF135748 UI-HF-BN0
c	602	18	1.1	654	8	BZ710282	BZ710282 OGBAK10TC
c	603	18	1.1	654	9	CE253252	CE253252 tigr-gss-
c	604	18	1.1	654	9	CG372743	CG372743 OG5BM63TC
	605	18	1.1	655	1	AU266512	AU266512 AU266512
c	606	18	1.1	655	8	BZ735612	BZ735612 OGEDU15TM
	607	18	1.1	656	6	CB132029	CB132029 K-EST0182
	608	18	1.1	656	8	AQ823074	AQ823074 HS_3191_A
	609	18	1.1	657	5	BU487149	BU487149 604127702
	610	18	1.1	658	5	BU488336	BU488336 604124941
c	611	18	1.1	658	9	CC622230	CC622230 OGUJQ29TH
c	612	18	1.1	659	8	BH271379	BH271379 CH230-19K
	613	18	1.1	660	5	BQ548523	BQ548523 rd32b06.y
c	614	18	1.1	660	8	BH391979	BH391979 AG-ND-106
c	615	18	1.1	661	1	AL600911	AL600911 DKFZp313N
c	616	18	1.1	661	2	AW949486	AW949486 EST361556
c	617	18	1.1	662	4	BG694829	BG694829 NISC_iv08
c	618	18	1.1	663	4	BM834378	BM834378 K-EST0109
	619	18	1.1	664	1	AU129912	AU129912 AU129912
c	620	18	1.1	665	4	BI755659	BI755659 603027011
c	621	18	1.1	665	4	BM827891	BM827891 K-EST0100
	622	18	1.1	665	8	BH256769	BH256769 CH230-286
c	623	18	1.1	666	7	CN105385	CN105385 EC2CAA27C
c	624	18	1.1	666	7	CR285990	CR285990 CR285990
	625	18	1.1	667	2	AW915530	AW915530 EST346834
	626	18	1.1	667	5	BU487079	BU487079 604127166
c	627	18	1.1	669	4	BM728921	BM728921 UI-E-EO1-
	628	18	1.1	669	4	BM860126	BM860126 fy34e07.y
c	629	18	1.1	673	4	BG432746	BG432746 602496138
	630	18	1.1	673	4	BJ506738	BJ506738 BJ506738
	631	18	1.1	674	5	BU490871	BU490871 604131841
	632	18	1.1	674	9	CE631033	CE631033 tigr-gss-
	633	18	1.1	675	5	BU396366	BU396366 603803267
	634	18	1.1	678	6	CA172751	CA172751 SCSGSB100
	635	18	1.1	680	8	CC164252	CC164252 ii84b11.b
	636	18	1.1	681	4	BJ539624	BJ539624 BJ539624
c	637	18	1.1	681	8	BZ015133	BZ015133 oei06h03.
c	638	18	1.1	683	8	BZ313517	BZ313517 hz08c12.b
	639	18	1.1	684	9	CL661532	CL661532 PRI013a_E
	640	18	1.1	685	4	BJ736859	BJ736859 BJ736859
	641	18	1.1	685	7	CK541797	CK541797 rswhb0_00
	642	18	1.1	686	1	AI968234	AI968234 wu14g01.x
c	643	18	1.1	686	6	CB031133	CB031133 TgESTzyd4
	644	18	1.1	686	6	CD803569	CD803569 UI-M-GV0-
	645	18	1.1	686	8	AZ973106	AZ973106 2M0247P07
c	646	18	1.1	686	8	BZ312767	BZ312767 id29c12.b
	647	18	1.1	687	9	CG350049	CG350049 OG5DN14TC
	648	18	1.1	689	2	BE407729	BE407729 601299773
c	649	18	1.1	689	7	CK937952	CK937952 CGF100447
	650	18	1.1	689	9	CE270912	CE270912 tigr-gss-
	651	18	1.1	691	2	BE787707	BE787707 601481849
	652	18	1.1	691	5	BM938634	BM938634 UI-M-CG0p
	653	18	1.1	691	8	BZ391904	BZ391904 EINDX01TF
c	654	18	1.1	693	5	BQ573457	BQ573457 UI-M-FD0-
c	655	18	1.1	693	6	CB124488	CB124488 K-EST0173
c	656	18	1.1	694	2	BE586150	BE586150 Est#9T7_G
	657	18	1.1	694	5	BU416688	BU416688 603551102
	658	18	1.1	694	5	BW072893	BW072893 BW072893
c	659	18	1.1	694	9	CC679479	CC679479 OGVEN74TH
	660	18	1.1	695	4	BJ736012	BJ736012 BJ736012
	661	18	1.1	696	5	BU489055	BU489055 604127535
	662	18	1.1	697	5	BU636292	BU636292 049B03 In
c	663	18	1.1	697	7	CN255844	CN255844 170004243
c	664	18	1.1	697	8	CC356960	CC356960 PUEEX62TD
	665	18	1.1	698	7	CF518449	CF518449 CAP0007_I
	666	18	1.1	698	8	BZ710299	BZ710299 OGBAK10TM
	667	18	1.1	699	8	BH677206	BH677206 BOMCK32TF
	668	18	1.1	699	8	AQ423264	AQ423264 CITBI-E1-
	669	18	1.1	701	5	BQ862314	BQ862314 QGC20M06.
	670	18	1.1	701	9	CR322075	CR322075 Medicago
	671	18	1.1	702	5	BQ617310	BQ617310 fab02g11.
c	672	18	1.1	702	9	CE372446	CE372446 tigr-gss-
	673	18	1.1	703	7	CK871716	CK871716 AGENCOURT
c	674	18	1.1	703	7	CO819406	CO819406 CSECS154A
c	675	18	1.1	704	5	BQ616989	BQ616989 fab02g11.
	676	18	1.1	704	5	BX312783	BX312783 BX312783
	677	18	1.1	704	9	AG345327	AG345327 Mus muscu
	678	18	1.1	706	4	BI654745	BI654745 603281772
	679	18	1.1	706	5	BU207209	BU207209 604159173
c	680	18	1.1	706	8	BZ514113	BZ514113 BOMRI16TF
	681	18	1.1	707	4	BI756284	BI756284 603024356

	682	18	1.1	707	8	BH967534	BH967534 odj32d10.
c	683	18	1.1	707	8	BZ198574	BZ198574 CH230-270
c	684	18	1.1	708	7	CK844347	CK844347 UI-R-BJ1-
	685	18	1.1	708	9	CR051344	CR051344 Forward s
	686	18	1.1	709	5	BU487467	BU487467 604124852
c	687	18	1.1	709	6	CB516136	CB516136 ssalrgb51
	688	18	1.1	711	9	CE458056	CE458056 tigr-gss-
c	689	18	1.1	712	4	BG483741	BG483741 602503379
	690	18	1.1	712	8	BH674678	BH674678 BOMAB28TR
	691	18	1.1	712	9	BX223222	BX223222 Danio rer
c	692	18	1.1	712	9	CE129718	CE129718 tigr-gss-
	693	18	1.1	713	7	CK024281	CK024281 AGENCOURT
	694	18	1.1	713	7	CK939714	CK939714 CGF100474
	695	18	1.1	715	5	BU486994	BU486994 604124804
c	696	18	1.1	716	2	BB367638	BB367638 BB367638
c	697	18	1.1	716	7	CO103472	CO103472 GR__Eb003
	698	18	1.1	717	5	BU488692	BU488692 604127605
c	699	18	1.1	717	7	CK707398	CK707398 ZF101-P00
c	700	18	1.1	717	8	BZ921766	BZ921766 CH240_119
	701	18	1.1	718	5	BU417494	BU417494 603671503
	702	18	1.1	719	7	CN057182	CN057182 Salamande
	703	18	1.1	719	7	CN294479	CN294479 170005313
	704	18	1.1	719	9	CE409861	CE409861 tigr-gss-
	705	18	1.1	720	7	CN294463	CN294463 170005830
	706	18	1.1	720	8	BZ327625	BZ327625 id29c12.g
c	707	18	1.1	720	9	CNS00X3A	AL094372 Arabidops
c	708	18	1.1	721	5	BX115485	BX115485 BX115485
c	709	18	1.1	721	7	CO074603	CO074603 GR__Ea34M
c	710	18	1.1	722	4	BJ625447	BJ625447 BJ625447
	711	18	1.1	722	5	BU417107	BU417107 603671414
c	712	18	1.1	722	7	CR427981	CR427981 CR427981
	713	18	1.1	724	5	BU488716	BU488716 604127187
	714	18	1.1	725	5	BU932504	BU932504 AGENCOURT
	715	18	1.1	725	6	CA429752	CA429752 UI-H-FH1-
c	716	18	1.1	726	9	CC723940	CC723940 OGVEP75TH
	717	18	1.1	727	5	BU487236	BU487236 604127173
c	718	18	1.1	727	9	CC636397	CC636397 OGCDF56TC
	719	18	1.1	728	5	BQ865166	BQ865166 QGC28O21.
	720	18	1.1	728	6	BY731748	BY731748 BY731748
	721	18	1.1	729	2	BE274857	BE274857 601122856
c	722	18	1.1	729	4	BM763262	BM763262 K-EST0044
	723	18	1.1	729	7	CN294472	CN294472 170004241
c	724	18	1.1	730	4	BI550734	BI550734 603195621
c	725	18	1.1	730	7	CF766764	CF766764 CES006001
c	726	18	1.1	731	5	BU465371	BU465371 603777709
	727	18	1.1	732	5	BU491813	BU491813 604131727
	728	18	1.1	732	7	CN755967	CN755967 ID0AAA17B
c	729	18	1.1	734	5	BP152942	BP152942 BP152942
	730	18	1.1	735	5	BU490541	BU490541 604131042
	731	18	1.1	735	7	CF444619	CF444619 EST680964
c	732	18	1.1	735	7	CN053640	CN053640 Salamande
c	733	18	1.1	736	1	AA967722	AA967722 uh04a09.r
	734	18	1.1	736	5	BX717524	BX717524 BX717524
c	735	18	1.1	736	9	AG444357	AG444357 Mus muscu
c	736	18	1.1	736	9	CG391711	CG391711 ZMMBBc057
c	737	18	1.1	736	9	AG182762	AG182762 Pan trogl
c	738	18	1.1	737	7	CN793801	CN793801 4128880 B
	739	18	1.1	737	9	CL652689	CL652689 PRI0115c_
	740	18	1.1	739	5	BX093469	BX093469 BX093469
c	741	18	1.1	739	9	CE151013	CE151013 tigr-gss-
	742	18	1.1	740	8	AZ244786	AZ244786 RPCI-23-4
	743	18	1.1	741	7	CK025140	CK025140 AGENCOURT
c	744	18	1.1	741	9	CL737593	CL737593 OR_BBa007
	745	18	1.1	742	9	CR007615	CR007615 Forward s
c	746	18	1.1	743	5	BP433720	BP433720 BP433720
	747	18	1.1	743	5	BU491238	BU491238 604130127
	748	18	1.1	743	5	BU491311	BU491311 604131280
	749	18	1.1	743	9	CC911055	CC911055 t064o20ba
c	750	18	1.1	744	1	AU141032	AU141032 AU141032
	751	18	1.1	744	5	BQ864656	BQ864656 QGC27F10.
	752	18	1.1	744	7	CK315763	CK315763 SB02026B2
	753	18	1.1	744	7	CO160352	CO160352 FLD1_20_A
c	754	18	1.1	744	9	CG252795	CG252795 OGXDY23TH
	755	18	1.1	745	9	CR342873	CR342873 Medicago
c	756	18	1.1	745	9	CL188661	CL188661 104_405_1
c	757	18	1.1	746	9	AG579279	AG579279 Mus muscu
	758	18	1.1	748	7	CK869636	CK869636 AGENCOURT
	759	18	1.1	748	7	CN206877	CN206877 Tor729 Ga
c	760	18	1.1	748	7	CN232583	CN232583 WLB050F02
	761	18	1.1	748	9	AG490663	AG490663 Mus muscu
	762	18	1.1	749	4	BJ507034	BJ507034 BJ507034
c	763	18	1.1	749	9	CC709181	CC709181 OGVEO40TH
	764	18	1.1	750	5	BQ863744	BQ863744 QGC24L15.
c	765	18	1.1	750	7	CN077364	CN077364 EC2BBA13B
	766	18	1.1	751	5	BU416346	BU416346 603551203
c	767	18	1.1	751	7	CR554523	CR554523 DKFZp459F
c	768	18	1.1	751	7	CR579660	CR579660 CR579660
c	769	18	1.1	751	8	BZ774503	BZ774503 mcv96a06.
	770	18	1.1	751	8	BZ959965	PUGEH36TB
c	771	18	1.1	751	9	CC634249	CC634249 OGVEO73TH
c	772	18	1.1	751	9	CL116908	CL116908 ISB1-66K1
c	773	18	1.1	752	4	BJ742816	BJ742816 BJ742816
	774	18	1.1	752	5	BU486944	BU486944 604126594
	775	18	1.1	752	7	CN170561	CN170561 AGENCOURT
	776	18	1.1	752	9	CC600200	ZMMBBc040
c	777	18	1.1	754	4	BJ748649	BJ748649 BJ748649
	778	18	1.1	754	7	CK305986	CK305986 SB02031B2
c	779	18	1.1	754	7	CO117100	CO117100 GR__Eb019
	780	18	1.1	756	4	BI254863	BI254863 602974129
	781	18	1.1	756	9	CR319091	CR319091 Medicago
c	782	18	1.1	756	9	CL159606	CL159606 104_349_1
c	783	18	1.1	757	9	CC610576	CC610576 OGVEP87TH
	784	18	1.1	758	7	CK866690	CK866690 AGENCOURT
	785	18	1.1	759	5	BU492046	BU492046 604132155
	786	18	1.1	759	7	CK869708	CK869708 AGENCOURT
c	787	18	1.1	760	8	BZ793280	BZ793280 PUGDO96TB
c	788	18	1.1	760	9	CC611230	CC611230 OGUDX27TV
	789	18	1.1	761	8	BZ973813	BZ973813 PUGHE16TB
c	790	18	1.1	762	4	BG967183	BG967183 602833863
	791	18	1.1	762	7	CK025010	CK025010 AGENCOURT
c	792	18	1.1	763	1	AL598882	AL598882 DKFZp313P
	793	18	1.1	763	7	CK127633	CK127633 AGENCOURT
c	794	18	1.1	764	4	BI310207	BI310207 EST531195
	795	18	1.1	764	8	AQ738662	AQ738662 HS_5381_B
	796	18	1.1	764	9	CG020419	CG020419 ZMMBBc055
c	797	18	1.1	765	6	CB092220	CB092220 hf02g08.g
c	798	18	1.1	765	9	AG566289	AG566289 Mus muscu
	799	18	1.1	766	7	CO246119	CO246119 AGENCOURT
	800	18	1.1	767	7	CK865671	CK865671 AGENCOURT
c	801	18	1.1	767	9	CC698147	CC698147 OGWEJ23TH
c	802	18	1.1	768	6	CA917697	CA917697 EST641844
c	803	18	1.1	768	8	BZ639917	BZ639917 OGCBV05TC
	804	18	1.1	769	9	CG276764	CG276764 OGWAQ80TH
	805	18	1.1	770	5	BU416685	BU416685 603670675
	806	18	1.1	770	7	CK127178	CK127178 AGENCOURT
	807	18	1.1	771	2	BF038815	BF038815 601462187
c	808	18	1.1	771	9	CC560438	CC560438 CH240_469
	809	18	1.1	772	7	CK127211	CK127211 AGENCOURT
c	810	18	1.1	772	9	CG256745	CG256745 OGYCP59TH
	811	18	1.1	773	7	CK873191	CK873191 AGENCOURT
	812	18	1.1	775	7	CK869731	CK869731 AGENCOURT
	813	18	1.1	776	7	CK142473	CK142473 AGENCOURT
c	814	18	1.1	776	7	CO101313	CO101313 GR__Eb002
	815	18	1.1	776	9	CG698678	ZMMBBc011
	816	18	1.1	777	7	CK872867	CK872867 AGENCOURT
c	817	18	1.1	777	8	BH321589	BH321589 CH230-104
	818	18	1.1	777	9	CC611222	CC611222 OGUDX27TH
	819	18	1.1	778	7	CK871227	CK871227 AGENCOURT
	820	18	1.1	778	8	BZ546495	BZ546495 OGAFC51TC
c	821	18	1.1	778	9	CC699800	CC699800 OGVEN87TH
	822	18	1.1	779	9	CL236331	CL236331 ZMMBBb057
	823	18	1.1	781	6	CB514418	CB514418 ssalrgb55
	824	18	1.1	782	5	BU488564	BU488564 604125056
c	825	18	1.1	782	8	BZ058247	BZ058247 ljr44b05.
	826	18	1.1	783	5	BP446124	BP446124 BP446124
	827	18	1.1	783	9	CR137453	CR137453 Forward s

c	828	18	1.1	783	9	CL015262	CL015262 ZMMBBb055
	829	18	1.1	786	7	CR579659	CR579659 CR579659
	830	18	1.1	786	8	BH322008	BH322008 CH230-20J
	831	18	1.1	786	9	CR215122	CR215122 Reverse s
c	832	18	1.1	787	9	CC491002	CC491002 CH240_324
	833	18	1.1	788	6	CA324116	CA324116 UI-M-FY0-
	834	18	1.1	788	7	CK864546	CK864546 AGENCOURT
	835	18	1.1	788	7	CN294471	CN294471 170005999
c	836	18	1.1	788	8	BZ405561	BZ405561 OGACX69TC
c	837	18	1.1	788	9	CC816129	CC816129 1O0001F06
c	838	18	1.1	791	8	CC420017	CC420017 PUHCF79TB
c	839	18	1.1	792	6	CA323239	CA323239 UI-M-FX0-
	840	18	1.1	793	7	CK869453	CK869453 AGENCOURT
	841	18	1.1	793	7	CK870425	CK870425 AGENCOURT
	842	18	1.1	793	7	CO248942	CO248942 AGENCOURT
	843	18	1.1	793	9	CG283240	CG283240 OGWIX65TH
	844	18	1.1	794	7	CN319691	CN319691 AGENCOURT
	845	18	1.1	795	4	BG566441	BG566441 602585250
	846	18	1.1	795	7	CK238544	CK238544 AGENCOURT
c	847	18	1.1	795	9	CG326506	CG326506 OGWJO11TH
c	848	18	1.1	796	1	AA711767	AA711767 vu58f10.r
c	849	18	1.1	800	8	BZ444120	BZ444120 BONJI01TR
	850	18	1.1	800	9	CG003933	CG003933 ZUAEG22TV
	851	18	1.1	801	2	BF794054	BF794054 602255612
	852	18	1.1	801	7	CK018357	CK018357 AGENCOURT
	853	18	1.1	801	9	CR084941	CR084941 Reverse s
c	854	18	1.1	801	9	CG321473	CG321473 OGVCT70TV
	855	18	1.1	802	7	CK142432	CK142432 AGENCOURT
	856	18	1.1	802	7	CK865171	CK865171 AGENCOURT
	857	18	1.1	804	7	CK870526	CK870526 AGENCOURT
	858	18	1.1	805	7	CO248796	CO248796 AGENCOURT
c	859	18	1.1	805	8	CC331820	CC331820 OGMBJ57TV
	860	18	1.1	806	4	BM043718	BM043718 603620524
	861	18	1.1	806	7	CK142957	CK142957 AGENCOURT
	862	18	1.1	807	7	CK127783	CK127783 AGENCOURT
	863	18	1.1	807	7	CK866332	CK866332 AGENCOURT
	864	18	1.1	807	7	CK869311	CK869311 AGENCOURT
	865	18	1.1	807	7	CK871919	CK871919 AGENCOURT
c	866	18	1.1	808	1	AL555563	AL555563 AL555563
	867	18	1.1	808	5	BU416963	BU416963 603671334
	868	18	1.1	808	7	CK870887	CK870887 AGENCOURT
	869	18	1.1	808	8	BZ722437	BZ722437 PUDAY11TD
	870	18	1.1	809	5	BU416777	BU416777 603671672
c	871	18	1.1	809	7	CO569288	CO569288 AGENCOURT
	872	18	1.1	810	4	BI259287	BI259287 602972518
	873	18	1.1	810	7	CK025907	CK025907 AGENCOURT
	874	18	1.1	810	9	CC698157	CC698157 OGWEJ23TV
	875	18	1.1	810	9	CG240660	CG240660 OG3BA81TH
c	876	18	1.1	810	9	CG920172	CG920172 MBEGQ24TR
	877	18	1.1	811	7	CR442119	CR442119 CR442119
c	878	18	1.1	811	9	CC610512	CC610512 OGULB25TH
	879	18	1.1	812	5	BU934601	BU934601 AGENCOURT
	880	18	1.1	812	7	CK867128	CK867128 AGENCOURT
	881	18	1.1	812	8	AZ675242	AZ675242 ENTJJ67TF
	882	18	1.1	813	9	CC675337	CC675337 OGMBB37TV
	883	18	1.1	814	5	BU416903	BU416903 603671255
	884	18	1.1	814	7	CK870281	CK870281 AGENCOURT
c	885	18	1.1	815	6	CD656211	CD656211 AGENCOURT
	886	18	1.1	816	9	CG261439	CG261439 OG0AX35TV
	887	18	1.1	817	8	CC342920	CC342920 OGRAC38TV
c	888	18	1.1	817	8	CC376274	CC376274 PUHCG81TB
	889	18	1.1	818	7	CK866929	CK866929 AGENCOURT
c	890	18	1.1	819	2	BE054345	BE054345 GA__Ea003
	891	18	1.1	819	5	BU747683	BU747683 CH3#014_G
	892	18	1.1	819	6	CB245112	CB245112 UI-M-FY0-
	893	18	1.1	820	2	BE744829	BE744829 601575058
c	894	18	1.1	820	5	BQ221812	BQ221812 AGENCOURT
c	895	18	1.1	820	9	CG249865	CG249865 OGWIS75TH
	896	18	1.1	824	4	BG610975	BG610975 602612279
	897	18	1.1	824	7	CK018308	CK018308 AGENCOURT
	898	18	1.1	825	7	CO363228	CO363228 RTK1_8_A0
c	899	18	1.1	825	7	CR579684	CR579684 CR579684
	900	18	1.1	826	7	CK015602	CK015602 AGENCOURT
	901	18	1.1	828	1	AU117565	AU117565 AU117565
	902	18	1.1	828	7	CK866292	CK866292 AGENCOURT
	903	18	1.1	829	7	CK869684	CK869684 AGENCOURT
	904	18	1.1	830	2	BF669601	BF669601 602120326
	905	18	1.1	830	5	BU417420	BU417420 603670591
c	906	18	1.1	830	8	BZ976530	BZ976530 PUGHO92TB
	907	18	1.1	831	7	CK872899	CK872899 AGENCOURT
	908	18	1.1	831	7	CN324421	CN324421 AGENCOURT
	909	18	1.1	831	9	CC840811	CC840811 ZMMBBc050
	910	18	1.1	832	2	BF576177	BF576177 602132612
	911	18	1.1	832	7	CK126714	CK126714 AGENCOURT
	912	18	1.1	832	7	CK142021	CK142021 AGENCOURT
c	913	18	1.1	832	8	BH361458	BH361458 CH230-164
c	914	18	1.1	832	9	CR199116	CR199116 Reverse s
c	915	18	1.1	833	9	CC477925	CC477925 CH240_304
c	916	18	1.1	834	8	CC198975	CC198975 ZMMBBc032
	917	18	1.1	834	8	CC420020	CC420020 PUHCF79TD
c	918	18	1.1	835	9	CC723962	CC723962 OGKAI11TH
	919	18	1.1	835	9	CG819566	CG819566 SOYFD75TV
c	920	18	1.1	836	7	CK016672	CK016672 AGENCOURT
	921	18	1.1	837	8	BZ599505	BZ599505 WHADP80TR
	922	18	1.1	837	8	CC196623	CC196623 ZMMBBc030
c	923	18	1.1	837	9	CC779986	CC779986 ZMMBBc043
	924	18	1.1	838	1	AU119855	AU119855 AU119855
	925	18	1.1	838	5	BU416852	BU416852 603671071
	926	18	1.1	838	5	BU417045	BU417045 603670568
	927	18	1.1	839	7	CK015462	CK015462 AGENCOURT
	928	18	1.1	839	7	CK015693	CK015693 AGENCOURT
	929	18	1.1	839	8	BZ979158	BZ979158 PUGIZ78TD
	930	18	1.1	840	5	BX415437	BX415437 BX415437
	931	18	1.1	840	9	CC721509	CC721509 OGMAY37TV
c	932	18	1.1	841	5	BU559231	BU559231 AGENCOURT
c	933	18	1.1	841	8	BH033674	BH033674 RPCI-24-3
	934	18	1.1	841	9	CR321373	CR321373 Medicago
	935	18	1.1	842	7	CK869709	CK869709 AGENCOURT
	936	18	1.1	842	9	CC580554	CC580554 CH240_375
	937	18	1.1	842	9	CC636402	CC636402 OGCDF56TM
	938	18	1.1	842	9	CG099564	CG099564 PUJFV79TB
c	939	18	1.1	842	9	CG789218	CG789218 ZMMBBb026
	940	18	1.1	843	7	CF663451	CF663451 RTCNT1_2_
c	941	18	1.1	845	9	CC494129	CC494129 CH240_329
	942	18	1.1	846	9	CC701583	CC701583 OGJAQ89TV
c	943	18	1.1	847	9	CC675325	CC675325 OGMBB37TH
	944	18	1.1	848	7	CK015811	CK015811 AGENCOURT
	945	18	1.1	848	7	CO814383	CO814383 AGENCOURT
	946	18	1.1	849	3	CNS0A3E4	BX829281 Arabidops
c	947	18	1.1	850	4	BG402418	BG402418 602466118
	948	18	1.1	850	4	BG468635	BG468635 602510235
c	949	18	1.1	850	8	BH598491	BH598491 BOGUI33TF
	950	18	1.1	851	9	CNS035G4	AL228685 Tetraodon
c	951	18	1.1	851	9	CC810512	CC810512 ZMMBBc047
	952	18	1.1	852	5	BU487262	BU487262 604126373
	953	18	1.1	852	7	CN323700	CN323700 AGENCOURT
c	954	18	1.1	852	9	CC721496	CC721496 OGMAY37TH
c	955	18	1.1	853	9	CG239425	CG239425 OGWLI58TH
c	956	18	1.1	854	5	BX701331	BX701331 BX701331
	957	18	1.1	854	7	CO248162	CO248162 AGENCOURT
c	958	18	1.1	854	9	CG068759	CG068759 PUIFC02TB
	959	18	1.1	855	7	CK864701	CK864701 AGENCOURT
c	960	18	1.1	855	9	CG276969	CG276969 OGYBC39TH
c	961	18	1.1	855	9	CG463804	CG463804 ZUAHL61TH
c	962	18	1.1	856	9	CC656134	CC656134 OGUEY79TV
	963	18	1.1	858	7	CK173598	CK173598 EST762918
	964	18	1.1	859	8	CC012684	CC012684 PUDGN23TD
	965	18	1.1	860	4	BI092380	BI092380 602856946
	966	18	1.1	860	7	CK872086	CK872086 AGENCOURT
	967	18	1.1	860	7	CK872580	CK872580 AGENCOURT
	968	18	1.1	860	7	CN316351	CN316351 AGENCOURT
c	969	18	1.1	862	5	BX410130	BX410130 BX410130
	970	18	1.1	863	7	CK015437	CK015437 AGENCOURT
	971	18	1.1	863	9	CG258635	CG258635 OGWAB02TH
c	972	18	1.1	864	3	CNS0A4FE	BX828029 Arabidops
	973	18	1.1	864	9	CC696021	CC696021 OGVAX24TV

974	18	1.1	867	7	CN167671	CN167671 AGENCOURT
975	18	1.1	867	8	BZ639922	BZ639922 OGCBV05TM
976	18	1.1	868	2	BE539135	BE539135 601061695
977	18	1.1	868	9	CG176984	CG176984 PUFQA70TD
c 978	18	1.1	869	4	BG531389	BG531389 602559640
979	18	1.1	870	7	CN326644	CN326644 AGENCOURT
980	18	1.1	871	6	CA496252	CA496252 AGENCOURT
981	18	1.1	872	4	BI858733	BI858733 603386325
982	18	1.1	872	7	CN320420	CN320420 AGENCOURT
983	18	1.1	873	7	CK872123	CK872123 AGENCOURT
c 984	18	1.1	873	9	CL725714	CL725714 OR_BBa005
985	18	1.1	874	7	CN330403	CN330403 AGENCOURT
986	18	1.1	875	2	BE570325	BE570325 601333205
987	18	1.1	875	8	BZ283509	BZ283509 CH230-286
988	18	1.1	875	9	CG249875	CG249875 OGWIS75TV
989	18	1.1	876	5	BU416923	BU416923 603670985
990	18	1.1	876	7	CN329994	CN329994 AGENCOURT
c 991	18	1.1	877	9	CC997475	CC997475 ZUABF94TH
992	18	1.1	878	5	BX400411	BX400411 BX400411
993	18	1.1	879	7	CN322875	CN322875 AGENCOURT
994	18	1.1	879	8	BZ742467	BZ742467 OGFCN24TC
995	18	1.1	879	9	CG335109	CG335109 OGZBI20TH
996	18	1.1	882	2	BF789402	BF789402 602103450
c 997	18	1.1	882	9	CC847013	CC847013 NDL.30C11
998	18	1.1	882	9	CG318903	CG318903 OG1DM50TH
999	18	1.1	883	7	CN323208	CN323208 AGENCOURT
c1000	18	1.1	883	8	CC141792	CC141792 NDL.51D20

ALIGNMENTS

RESULT 1
AU237072
LOCUS AU237072 596 bp mRNA linear EST 01-APR-2002
DEFINITION AU237072 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-47-A08 5', mRNA sequence.
ACCESSION AU237072
VERSION AU237072.1 GI:19876241
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 596)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
FEATURES Location/Qualifiers
source 1. .596
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL15-47-A08"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL15"
/note="Site_1: BamHI; Site_2: SalI"
ORIGIN

Query Match 25.0%; Score 410; DB 1; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.2e-221;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 169

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 229

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 289

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        290 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 349

Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 409

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 469

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCT 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCT 519
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RESULT 2
BH944186
LOCUS BH944186 625 bp DNA linear GSS 01-OCT-2002
DEFINITION obu90a02.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BH944186
VERSION BH944186.1 GI:23424246
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 625)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: obu90 row: a column: 02
Seq primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 45
High quality sequence stop: 398.
FEATURES Location/Qualifiers
source 1. .625
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 4.0%; Score 65; DB 8; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        586 ATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAA 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 ATGGGTAATAATGTCTTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAA 406

Qy        646 CATTA 650
              |||||
Db        407 CATTA 411
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RESULT 3
CC948085
LOCUS CC948085 546 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIHF12TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone BOIHF12, genomic survey sequence.
ACCESSION CC948085
VERSION CC948085.1 GI:33782462
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 546)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOIHF12TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .546
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIHF12"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: pHOS2; Site_1: BstXI; 1.4-1.6 kb sheared nuclear DNA inserted into pHOS2 using BstXI linkers"
ORIGIN

Query Match 3.5%; Score 58; DB 9; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        715 GTTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGG 772
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GTTGAGGCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGG 306
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RESULT 4
AJ589191/c
LOCUS AJ589191 249 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 361B03, genomic survey sequence.
ACCESSION AJ589191
VERSION AJ589191.1 GI:37938815
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 249)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .249
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="361B03"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .249
/note="T-DNA flanking sequence left border"
ORIGIN

Query Match 3.5%; Score 57; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1336 AGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTA 1392
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 AGGTCTGGAACTGTGGTTGATGGGAACGCTGGACCTATAACTGGGGATGAGACGGTA 134
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RESULT 5
BZ082259
LOCUS BZ082259 703 bp DNA linear GSS 10-OCT-2002
DEFINITION lkv30d04.b1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.
ACCESSION BZ082259
VERSION BZ082259.1 GI:23708975
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 703)
AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)

```
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: 1kv30  row: d  column: 04
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 77
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             3.5%;  Score 57;  DB 8;  Length 703;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-20;
  Matches   57;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1174 CTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCTCAT 1230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 CTGACTCCTTGGGAGAGACCACCTATAAAAAATGTATTTTGCATATATGGTGCTCAT 148


RESULT 6
BH974466/c
LOCUS       BH974466                673 bp    DNA     linear   GSS 02-OCT-2002
DEFINITION  odj06g04.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
            sequence.
ACCESSION   BH974466
VERSION     BH974466.1  GI:23457469
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 673)
  AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
            Nash,W., Rabinowicz,P.D. and Wilson,R.K.
  TITLE     Whole genome shotgun reads from Brassica oleracea
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Plate: odj06  row: g  column: 04
            Seq primer: -21UPpOT forward
            Class: shotgun
            High quality sequence start: 16
            High quality sequence stop: 551.
FEATURES             Location/Qualifiers
     source          1. .673
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone_lib="B.oleracea002"
                     /note="Vector: pOTw13; Whole genome shotgun library from
                     flowering buds. DNA was purified  from a crude nuclear
                     prep using Brassica oleracea TO1000DH3 buds  provided by
                     Thosmas Osborn at the University of Wisconsin. Genomic
                     DNA was provided by Pablo Rabinowicz (CSHL) and the
                     shotgun library  prepared at Washington University Genome
                     Sequencing Center."
ORIGIN

  Query Match             2.9%;  Score 47;  DB 8;  Length 673;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-14;
  Matches   47;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1249 TATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATCAT 1295
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Db        570 TATTACTTTGCCCCAAGTGGCAAACCTTATCCTGATAATTGGATCAT 524


RESULT 7
BH864615/c
LOCUS       BH864615                  40 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_096352 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_096352, genomic survey sequence.
ACCESSION   BH864615
VERSION     BH864615.1  GI:22100513
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At1g04010.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_096352"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             2.4%;  Score 40;  DB 8;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 AATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCG 49
              ||||||||||||||||||||||||||||||||||||||||
Db         40 AATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCG 1


RESULT 8
BH847141/c
LOCUS       BH847141                  70 bp    DNA     linear   GSS 13-JUN-2002
DEFINITION  SALK_013495.53.90.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_013495.53.90.x, genomic
            survey sequence.
ACCESSION   BH847141
```

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VERSION     BH847141.1  GI:21418012
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At1g04010.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_013495.53.90.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             2.0%;  Score 33;  DB 8;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-06;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1459 CAGCCAGAACACGATGGAAGCGACGTACATGTG 1491
              |||||||||||||||||||||||||||||||||
Db         33 CAGCCAGAACACGATGGAAGCGACGTACATGTG 1


RESULT 9
BH746163
LOCUS       BH746163                207 bp    DNA     linear   GSS 25-FEB-2002
DEFINITION  qo78e11.b1 BoBuds01 Brassica oleracea genomic clone qo78e11 5',
            genomic survey sequence.
ACCESSION   BH746163
VERSION     BH746163.1  GI:18881051
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Katari,M., O'Shaughnessy,A., Palmer,L., Bahret,A., Baker,J.,
            Balija,V., Cunnius,D.M., Katzenberger,P., King,L., Kirchoff,K.,
            Kuit,K., Miller,B., Muller,S., Nascimento,L., Preston,R.,
            Santos,L., Shah,R., Zutavern,T., Dedhia,N., Rabinowicz,P.D. and
            McCombie,W.R.
  TITLE     Whole Genome Shotgun Reads from Brassica oleracia (2002b)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Plate: qo78  row: e  column: 11
            Seq primer: -21UnivFwd
            Class: shotgun
            High quality sequence stop: 207.
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3712"
                     /clone="qo78e11"
                     /clone_lib="BoBuds01"
                     /note="Vector: M13 for .x reads, pBluescript for .b and .g
                     reads; Site_1: EcoRV; Whole genome shotgun library from
                     flowering buds. DNA was purified from a crude nuclear prep
                     using Brassica oleracea TO1000DH3 buds provided by Thomas
                     Osborn at the University of Wisconsin. Genomic DNA
                     provided by Pablo Rabinowicz (CSHL) and shotgun library
                     prepared in McCombie Lab."
ORIGIN

  Query Match             2.0%;  Score 32;  DB 8;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-06;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        586 ATGGGTAATAATGTCTTCAGATACTTTCTGGA 617
              ||||||||||||||||||||||||||||||||
Db        118 ATGGGTAATAATGTCTTCAGATACTTTCTGGA 149


RESULT 10
AU306500
LOCUS       AU306500                728 bp    mRNA    linear   EST 22-JAN-2004
DEFINITION  AU306500 zinnia cultured mesophyll cell equalized cDNA Zinnia
            elegans cDNA clone Z16086, mRNA sequence.
ACCESSION   AU306500
VERSION     AU306500.1  GI:41122436
KEYWORDS    EST.
SOURCE      Zinnia elegans
  ORGANISM  Zinnia elegans
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Zinnia.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Demura,T., Tashiro,G., Horiguchi,G., Kishimoto,N., Kubo,M.,
            Matsuoka,N., Minami,A., Nagata-Hiwatashi,M., Nakamura,K.,
            Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
            Fukuda,H.
  TITLE     Visualization by comprehensive microarray analysis of gene
            expression programs during transdifferentiation of mesophyll cells
            into xylem cells
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
COMMENT     Contact: Taku Demura
            Morphogenesis Research Group
            RIKEN Plant Science Center
            1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9605
            Fax: 81-45-503-9573
            Email: demura@postman.riken.go.jp
            This clone was obtained at our laboratory
            Seq primer: M13 forward.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Zinnia elegans"
                     /mol_type="mRNA"
                     /cultivar="Canary bird"
                     /db_xref="taxon:34245"
                     /clone="Z16086"
                     /tissue_type="mesophyll cell"
```

```
                     /clone_lib="zinnia cultured mesophyll cell equalized cDNA"
                     /note="Vector: pGEM-T easy; cultured in tracheary element
                     differentiation-inductive medium"
ORIGIN

  Query Match             1.8%;  Score 30;  DB 1;  Length 728;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 GCTGTTGGAGCTCCTCTTCTTGGTTCTGTT 717
              ||||||||||||||||||||||||||||||
Db        249 GCTGTTGGAGCTCCTCTTCTTGGTTCTGTT 278


RESULT 11
BH548609/c
LOCUS       BH548609                 303 bp    DNA     linear   GSS 14-DEC-2001
DEFINITION  BOHCO62TF BOHC Brassica oleracea genomic clone BOHCO62, genomic
            survey sequence.
ACCESSION   BH548609
VERSION     BH548609.1  GI:17800389
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 303)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOHCO62TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .303
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOHCO62"
                     /clone_lib="BOHC"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

  Query Match             1.8%;  Score 29;  DB 8;  Length 303;
  Best Local Similarity   100.0%;  Pred. No. 0.00035;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        403 GAGTGGCTTAAGTGGTGTGTTGAGTTTGG 431
              |||||||||||||||||||||||||||||
Db        212 GAGTGGCTTAAGTGGTGTGTTGAGTTTGG 184


RESULT 12
B11175
LOCUS       B11175                  1225 bp    DNA     linear   GSS 14-MAY-1997
DEFINITION  F14L4-Sp6 IGF Arabidopsis thaliana genomic clone F14L4, genomic
            survey sequence.
ACCESSION   B11175
VERSION     B11175.1  GI:2092305
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1225)
  AUTHORS   Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
            Ecker,J.
  TITLE     BAC End Sequences at ATGC
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: F14L4-T7
            Contact: Ecker J.
            Arabidopsis Thaliana Genome Center
            University of Pennsylvania
            Dept. of Biology, University of Pennsylvania, Philadelphia, PA
            19104
            Tel: 215-898-9384
            Fax: 215-898-8780
            Email: jecker@atgenome.bio.upenn.edu
            Seq primer: Sp6
            Class: BAC ends
            High quality sequence start: 155
            High quality sequence stop: 221.
FEATURES             Location/Qualifiers
     source          1. .1225
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="F14L4"
                     /sex="hermaphrodite"
                     /clone_lib="IGF"
                     /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
                     Produced by Thomas Altmann"
ORIGIN

  Query Match             1.7%;  Score 28;  DB 8;  Length 1225;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        165 AGCGTGGTCGATCCTTGACTGTCCATAC 192
              ||||||||||||||||||||||||||||
Db        209 AGCGTGGTCGATCCTTGACTGTCCATAC 236


RESULT 13
BI922233
LOCUS       BI922233                 632 bp    mRNA    linear   EST 17-OCT-2001
DEFINITION  EST542136 tomato callus Lycopersicon esculentum cDNA clone
            cLEC76P18 5' end, mRNA sequence.
ACCESSION   BI922233
VERSION     BI922233.1  GI:16218653
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 632)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A.,
            Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M.,
            Martin,G.B., Tanksley,S.D. and Giovannoni,J.
  TITLE     Generation of ESTs from tomato callus tissue (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            This clone is available through the Clemson University Genomics
            Institute
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .632
                     /organism="Lycopersicon esculentum"
                     /mol_type="mRNA"
```

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                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cLEC76P18"
                     /tissue_type="callus"
                     /dev_stage="25-40 days old"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="tomato callus"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Boyce Thompson Institute; sequencing: The
                     Institute for Genomic Research; cLEC - Cotyledons of
                     seedlings 7-10 days post-germination were excised, cut at
                     both ends and placed on MS medium with no selection. Mixed
                     callus was harvested at 25 and 40 days and included
                     undifferentiated masses. Tomato Callus EST Library"
ORIGIN

  Query Match             1.5%;  Score 24;  DB 4;  Length 632;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 GCTGTTGGAGCTCCTCTTCTTGGT 711
              ||||||||||||||||||||||||
Db        540 GCTGTTGGAGCTCCTCTTCTTGGT 563


RESULT 14
BI422757
LOCUS       BI422757                704 bp    mRNA    linear   EST 16-AUG-2001
DEFINITION  EST533423 tomato callus, TAMU Lycopersicon esculentum cDNA clone
            cLEC71F15 5' end, mRNA sequence.
ACCESSION   BI422757
VERSION     BI422757.1  GI:15197439
KEYWORDS    EST.
SOURCE      Lycopersicon esculentum (tomato)
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
            Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
            Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
            Giovannoni,J.
  TITLE     Generation of ESTs from tomato callus tissue
  JOURNAL   Unpublished (1999)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES             Location/Qualifiers
     source          1. .704
                     /organism="Lycopersicon esculentum"
                     /mol_type="mRNA"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cLEC71F15"
                     /tissue_type="callus"
                     /dev_stage="25-40 days old"
                     /lab_host="XL1-Blue MRF'"
                     /clone_lib="tomato callus, TAMU"
                     /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                     Xho1; supplier: Giovannoni laboratory; cLEC - Cotyledons
                     of seedlings 7-10 days post-germination were excised, cut
                     at both ends and placed on MS medium with no selection.
                     Mixed callus was harvested at 25 and 40 days and included
                     undifferentiated masses. Tomato Callus EST Library"
ORIGIN

  Query Match             1.5%;  Score 24;  DB 4;  Length 704;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 GCTGTTGGAGCTCCTCTTCTTGGT 711
              ||||||||||||||||||||||||
Db        540 GCTGTTGGAGCTCCTCTTCTTGGT 563


RESULT 15
CK259393
LOCUS       CK259393                788 bp    mRNA    linear   EST 03-AUG-2004
DEFINITION  EST705471 potato abiotic stress cDNA library Solanum tuberosum cDNA
            clone POAB029 5' end, mRNA sequence.
ACCESSION   CK259393
VERSION     CK259393.1  GI:39816371
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
  TITLE     Generation of ESTs from abiotic stressed potato tissue
  JOURNAL   Unpublished (2003)
COMMENT     Other_ESTs: EST705470 EST705472 EST705473
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from the University of Arizona Genomics
            Institute via http://genome.arizona.edu/orders/ .
            Seq primer: ATT TAG GTG ACA CTA TAG.
FEATURES             Location/Qualifiers
     source          1. .788
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="POAB029"
                     /tissue_type="abiotic stress treated leaf and root tissue"
                     /lab_host="DH10B-TonA"
                     /clone_lib="potato abiotic stress cDNA library"
                     /note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
                     supplier: Solanum tuberosum var. Kennebec plants were
                     grown from cuttings on a 16hr light/8 hr dark cycle at 25
                     C for 3-4 weeks. Abiotic stress conditions were applied to
                     four separate sets of plants. Set 1 involved saturation of
                     the soil with 150 mM NaCl and tissues were harvested at
                     following application of the salt stress (leaves: 2hr,
                     6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
                     Set 2 were grown under the standard conditions and then
                     were water stressed by withdrawal of further watering
                     applications. Drought stressed plants were harvested after
                     cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
                     and 5d). Set 3 were grown under the standard conditions
                     and then were cold stressed by placement at 4 C. Cold
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d. Set 4 were grown under the standard conditions and
                     then were heat stressed by placement at 35 C. Heat
                     stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
                     2d and 4d and heat-stressed roots were harvested at 6 hr,
                     12 hr, 1 d, and 4d. RNA was isolated from all tissues and
                     equal RNA from each tissue and stress was pooled to
                     construct the cDNA library. RNA sample."
ORIGIN

  Query Match             1.5%;  Score 24;  DB 7;  Length 788;
  Best Local Similarity   100.0%;  Pred. No. 0.27;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        688 GCTGTTGGAGCTCCTCTTCTTGGT 711
              ||||||||||||||||||||||||
Db         11 GCTGTTGGAGCTCCTCTTCTTGGT 34
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Search completed: November 9, 2004, 10:07:44
Job time : 5505 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2004, 02:27:12 ; Search time 7038 Seconds
(without alignments)
11026.200 Million cell updates/sec

Title: US-09-651-651-4
Perfect score: 1641
Sequence: 1 atgggagcgaattcgaaatc.....ttgataaaagtgggtattaa 1641

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1641	100.0	1641	6	AX090311	AX090311 Sequence
2		243	14.8	3896	6	BD271623	BD271623 Novel cla
3		243	14.8	3896	6	BD271633	BD271633 Novel cla
4		243	14.8	3896	6	AX037587	AX037587 Sequence
5		243	14.8	3896	6	AX037606	AX037606 Sequence
6		243	14.8	119914	8	AC003027	AC003027 Arabidops
7		27	1.6	44	6	AX090361	AX090361 Sequence
8	c	26	1.6	40	6	AX090362	AX090362 Sequence
9		25	1.5	2609	8	AF493159	AF493159 Medicago
10		21	1.3	2638	3	TRBVSGAAB	M16036 T.brucei va
11	c	21	1.3	38785	9	AC073993	AC073993 Homo sapi
12	c	21	1.3	70206	5	AL929207	AL929207 Zebrafish
13		21	1.3	74349	9	AL603869	AL603869 Human DNA
14	c	21	1.3	93398	8	AP006356	AP006356 Lotus cor
15		21	1.3	107430	9	AC006988	AC006988 Homo sapi
16	c	21	1.3	110000	2	BX813304_0	BX813304 Danio rer
17	c	21	1.3	119797	2	AC013236	AC013236 Drosophil
18	c	21	1.3	128623	3	AC092245	AC092245 Drosophil
19		21	1.3	134866	10	AL844206	AL844206 Mouse DNA
20	c	21	1.3	150797	2	CR352294	CR352294 Danio rer
21		21	1.3	174974	3	AC092228	AC092228 Drosophil
22		21	1.3	186945	2	AC111427	AC111427 Rattus no
23		21	1.3	192586	10	AL645972	AL645972 Mouse DNA
24		21	1.3	210702	5	BX119982	BX119982 Zebrafish
25		21	1.3	215899	5	BX004818	BX004818 Zebrafish
26	c	21	1.3	223940	2	AC087567	AC087567 Mus muscu
27	c	21	1.3	228999	2	AC083885	AC083885 Homo sapi
28		21	1.3	263309	3	AE003644	AE003644 Drosophil
29		21	1.3	300962	3	DROSADH04	AE003410 Drosophil
30	c	20	1.2	427	11	G61455	G61455 SHGC-85644
31	c	20	1.2	595	11	BV067360	BV067360 S209P6185
32	c	20	1.2	1667	14	HHU06940	U06940 Human herpe
33		20	1.2	7768	1	AF041837	AF041837 Buchnera
34		20	1.2	10242	1	AE000827	AE000827 Methanoba
35		20	1.2	25403	3	U64609	U64609 Caenorhabdi
36		20	1.2	63902	1	AY258503	AY258503 Escherich
37	c	20	1.2	75145	9	HS362G17	Z82204 Human DNA s
38		20	1.2	80182	5	AL772356	AL772356 Zebrafish
39		20	1.2	85905	2	AC133571	AC133571 Medicago
40		20	1.2	92799	2	AC135817	AC135817 Rattus no
41	c	20	1.2	93533	5	AL672129	AL672129 Zebrafish
42	c	20	1.2	96694	9	AC090470	AC090470 Homo sapi
43	c	20	1.2	110000	2	AP006500_09	Continuation (10 o
44	c	20	1.2	110695	9	AC010306	AC010306 Homo sapi
45	c	20	1.2	110758	8	AC147774	AC147774 Medicago
46		20	1.2	112027	9	AC073502	AC073502 Homo sapi
47	c	20	1.2	115626	9	AC103792	AC103792 Homo sapi
48		20	1.2	122897	2	AP001953	AP001953 Homo sapi
49	c	20	1.2	136228	2	AC067916	AC067916 Homo sapi
50	c	20	1.2	137278	10	AC104103	AC104103 Mus muscu
51		20	1.2	140547	2	AC147821	AC147821 Xenopus t
52	c	20	1.2	145728	5	AL935292	AL935292 Zebrafish
53	c	20	1.2	146245	2	AC148388	AC148388 Rhinoloph
54		20	1.2	147544	2	AC135325	AC135325 Homo sapi
55	c	20	1.2	148845	9	HS1114A1	AL035684 Human DNA
56		20	1.2	149879	2	AP005381	AP005381 Oryza sat
57	c	20	1.2	157093	2	AC006916	AC006916 Caenorhab
58		20	1.2	157797	8	AP005184	AP005184 Oryza sat
59		20	1.2	158792	8	AP003833	AP003833 Oryza sat
60		20	1.2	160869	2	AC147815	AC147815 Xenopus t
61		20	1.2	163183	9	AC016574	AC016574 Homo sapi
62	c	20	1.2	166651	4	AC087160	AC087160 Sus scrof
63		20	1.2	167137	2	AC150859	AC150859 Bos tauru
64		20	1.2	169588	8	AP006461	AP006461 Oryza sat
65	c	20	1.2	170777	2	AC148444	AC148444 Rhinoloph
66		20	1.2	171375	9	CNS01DSX	AL122023 Human chr
67		20	1.2	171877	2	BX928757	BX928757 Danio rer
68	c	20	1.2	171940	2	AC148514	AC148514 Papio anu
69		20	1.2	174147	2	AC148048	AC148048 Otolemur
70		20	1.2	175326	9	CNS01DTQ	AL132838 Human chr
71		20	1.2	176259	2	CR678095	CR678095 Danio rer
72		20	1.2	178157	2	AC101748	AC101748 Mus muscu
73	c	20	1.2	183298	2	AC101809	AC101809 Mus muscu
74		20	1.2	184266	2	BX571737	BX571737 Danio rer
75		20	1.2	185397	2	AC148555	AC148555 Callithri
76	c	20	1.2	185967	2	BX640499	BX640499 Danio rer
77		20	1.2	188333	9	AC016721	AC016721 Homo sapi
78	c	20	1.2	189927	10	AC116588	AC116588 Mus muscu
79		20	1.2	192252	2	AC148944	AC148944 Gasterost
80		20	1.2	194974	2	AC027105	AC027105 Homo sapi
81	c	20	1.2	195033	9	AC139362	AC139362 Homo sapi
82	c	20	1.2	196918	9	AC087463	AC087463 Homo sapi
83	c	20	1.2	197273	9	AC002461	AC002461 Homo sapi
84	c	20	1.2	197351	2	AC026092	AC026092 Homo sapi
85		20	1.2	200361	10	AC139241	AC139241 Mus muscu
86	c	20	1.2	200875	2	BX324158	BX324158 Danio rer
87	c	20	1.2	202972	10	AL663052	AL663052 Mouse DNA
88		20	1.2	210466	9	AC146059	AC146059 Pan trogl
89		20	1.2	232923	2	AC094246	AC094246 Rattus no
90		20	1.2	234744	5	AL935307	AL935307 Zebrafish
91		20	1.2	234826	2	AC093340	AC093340 Mus muscu
92	c	20	1.2	234909	2	AC094325	AC094325 Rattus no

93	20	1.2	240901	2	AC096328	AC096328 Rattus no
c 94	20	1.2	246877	2	AC137365	AC137365 Rattus no
c 95	20	1.2	250510	2	AC098055	AC098055 Rattus no
96	20	1.2	255349	2	AC095800	AC095800 Rattus no
c 97	20	1.2	256219	2	AC095416	AC095416 Rattus no
c 98	20	1.2	256220	2	AC109981	AC109981 Rattus no
99	20	1.2	265773	2	AC106686	AC106686 Rattus no
c 100	20	1.2	273684	2	AC113630	AC113630 Rattus no
c 101	20	1.2	294461	2	AC108628	AC108628 Rattus no
102	19	1.2	442	10	MUSAHR05	L19752 Mouse DNA s
c 103	19	1.2	571	11	BV036511	BV036511 S212P6019
c 104	19	1.2	675	6	CQ714589	CQ714589 Sequence
105	19	1.2	677	10	RATCPA4	M23987 Rat carboxy
106	19	1.2	1310	10	RNCPPA	V01232 Rat messeng
107	19	1.2	1337	4	BTCARPEP	Z33906 B.taurus mR
108	19	1.2	1362	4	BOVCARBPA	M61851 Bos taurus
109	19	1.2	1607	10	RATCBXPA	J00713 rat carboxy
110	19	1.2	1775	10	BC055778	BC055778 Mus muscu
111	19	1.2	1785	8	HTOTUBBET2	L39132 Histoplasma
c 112	19	1.2	2372	6	CQ796156	CQ796156 Sequence
c 113	19	1.2	2372	6	CQ796157	CQ796157 Sequence
c 114	19	1.2	2372	6	CQ796158	CQ796158 Sequence
c 115	19	1.2	2372	6	CQ796159	CQ796159 Sequence
c 116	19	1.2	2372	6	CQ796160	CQ796160 Sequence
c 117	19	1.2	2372	6	CQ796161	CQ796161 Sequence
c 118	19	1.2	2372	6	CQ796162	CQ796162 Sequence
c 119	19	1.2	2372	6	CQ796163	CQ796163 Sequence
c 120	19	1.2	2372	6	CQ796164	CQ796164 Sequence
c 121	19	1.2	2372	6	CQ796165	CQ796165 Sequence
c 122	19	1.2	2372	6	CQ796166	CQ796166 Sequence
c 123	19	1.2	2372	6	CQ796167	CQ796167 Sequence
c 124	19	1.2	2372	6	CQ796168	CQ796168 Sequence
c 125	19	1.2	2372	6	CQ796169	CQ796169 Sequence
c 126	19	1.2	2372	6	CQ796170	CQ796170 Sequence
c 127	19	1.2	2372	6	CQ796171	CQ796171 Sequence
c 128	19	1.2	2372	6	CQ796172	CQ796172 Sequence
c 129	19	1.2	2372	6	CQ796173	CQ796173 Sequence
c 130	19	1.2	2372	6	CQ796174	CQ796174 Sequence
c 131	19	1.2	2372	6	CQ796175	CQ796175 Sequence
c 132	19	1.2	2372	6	CQ796176	CQ796176 Sequence
133	19	1.2	2488	6	AR353989	AR353989 Sequence
134	19	1.2	2522	10	BC033430	BC033430 Mus muscu
135	19	1.2	3111	8	AK073117	AK073117 Oryza sat
c 136	19	1.2	3642	3	AY344240	AY344240 Trypanoso
137	19	1.2	4123	9	HUMMH1TRAN	J00191 Human MHC c
c 138	19	1.2	4745	9	HSM803666	AL832358 Homo sapi
c 139	19	1.2	6010	9	HSM804621	AL833308 Homo sapi
140	19	1.2	6142	8	CMRDNAI	X13059 Curcurbita
141	19	1.2	6142	8	CUCRGIS	M28700 C.maxima 26
142	19	1.2	6581	9	HUMMHANTLE	M31944 Human MHC c
c 143	19	1.2	8500	9	HSA292348	AJ292348 Homo sapi
144	19	1.2	8652	1	CBNMRSA	X77919 C.burnetti
c 145	19	1.2	17500	2	AC017179	AC017179 Drosophil
146	19	1.2	29774	1	AF193754	AF193754 Zymomonas
147	19	1.2	39108	9	BX284699	BX284699 Human DNA
c 148	19	1.2	41203	9	AC004194	AC004194 Homo sapi
c 149	19	1.2	51691	1	AC074318	AC074318 Staphyloc
150	19	1.2	58431	1	AC025591	AC025591 Staphyloc
c 151	19	1.2	62282	9	AC010304	AC010304 Homo sapi
152	19	1.2	62350	9	AC067725	AC067725 Homo sapi
153	19	1.2	66893	2	AC105793_5	Continuation (6 of
154	19	1.2	70206	2	AC126804_3	Continuation (4 of
c 155	19	1.2	74298	8	AB020745	AB020745 Arabidops
c 156	19	1.2	76880	2	AC150175	AC150175 Gallus ga
c 157	19	1.2	81561	9	AB023057	AB023057 Homo sapi
158	19	1.2	87397	9	AL356778	AL356778 Human DNA
c 159	19	1.2	88619	9	AC097723	AC097723 Homo sapi
160	19	1.2	88746	9	AC009321	AC009321 Homo sapi
c 161	19	1.2	90872	2	AC006940	AC006940 Drosophil
c 162	19	1.2	92586	2	AC005978	AC005978 Drosophil
163	19	1.2	94212	2	AC150246	AC150246 Medicago
164	19	1.2	95169	8	AP006084	AP006084 Lotus cor
165	19	1.2	95379	9	AC106749	AC106749 Homo sapi
c 166	19	1.2	100000	9	AP000520	AP000520 Homo sapi
c 167	19	1.2	101281	2	AC026389	AC026389 Homo sapi
c 168	19	1.2	104017	9	AC105050	AC105050 Homo sapi
169	19	1.2	105633	9	AL671561	AL671561 Human DNA
170	19	1.2	107164	9	AL449105	AL449105 Human DNA
c 171	19	1.2	110000	1	AE017225_45	Continuation (46 o
c 172	19	1.2	110000	1	AE017334_45	Continuation (46 o
c 173	19	1.2	110000	1	AE017355_45	Continuation (46 o
174	19	1.2	110000	1	AP003358_2	Continuation (3 of
175	19	1.2	110000	1	BX571856_02	Continuation (3 of
c 176	19	1.2	110000	2	AC091446_2	Continuation (3 of
177	19	1.2	110000	2	AC105793_4	Continuation (5 of
c 178	19	1.2	110000	2	CEY105E8_4	Continuation (5 of
c 179	19	1.2	110000	2	LMFLCHR26_0	AL160493 Leishmani
180	19	1.2	112242	9	AC004741	AC004741 Homo sapi
c 181	19	1.2	114707	2	AC146332	AC146332 Medicago
c 182	19	1.2	118192	8	AP004120	AP004120 Oryza sat
183	19	1.2	121341	10	BX005469	BX005469 Mouse DNA
c 184	19	1.2	123078	8	AP004902	AP004902 Lotus cor
185	19	1.2	125405	9	BX927141	BX927141 Human DNA
c 186	19	1.2	128757	2	AC142568	AC142568 Felis cat
c 187	19	1.2	129516	8	ATF24M12	AL132980 Arabidops
188	19	1.2	129611	9	AL645935	AL645935 Human DNA
c 189	19	1.2	130558	2	AC148793	AC148793 Otolemur
190	19	1.2	131368	9	CR388220	CR388220 Human DNA
191	19	1.2	131860	2	AC102708	AC102708 Mus muscu
c 192	19	1.2	132775	2	AC046156	AC046156 Homo sapi
c 193	19	1.2	132875	8	AC135461	AC135461 Medicago
c 194	19	1.2	133176	2	AC138445	AC138445 Felis cat
195	19	1.2	134019	3	AC006471	AC006471 Drosophil
196	19	1.2	137072	2	AL353893	AL353893 Homo sapi
197	19	1.2	137924	2	AC026684	AC026684 Homo sapi
198	19	1.2	139215	8	AC126780	AC126780 Medicago
c 199	19	1.2	139793	9	AC125629	AC125629 Homo sapi
c 200	19	1.2	140739	9	AP005432	AP005432 Homo sapi
201	19	1.2	142152	2	AC139658	AC139658 Rattus no
c 202	19	1.2	143461	2	AC141021	AC141021 Rattus no
203	19	1.2	144759	9	HS352A20	AL021939 Human DNA
204	19	1.2	145458	2	AC069591	AC069591 Homo sapi
c 205	19	1.2	146204	9	AC009316	AC009316 Homo sapi
c 206	19	1.2	147094	5	AL929543	AL929543 Zebrafish
c 207	19	1.2	147123	8	AP005691	AP005691 Oryza sat
208	19	1.2	147974	2	AC076970	AC076970 Homo sapi
209	19	1.2	148438	9	AC019072	AC019072 Homo sapi
c 210	19	1.2	149132	8	AC116949	AC116949 Oryza sat
211	19	1.2	150407	2	AC093228	AC093228 Homo sapi
212	19	1.2	151944	2	AC137701	AC137701 Medicago
c 213	19	1.2	152877	9	AC107399	AC107399 Homo sapi
c 214	19	1.2	154434	5	BX649404	BX649404 Zebrafish
c 215	19	1.2	154733	2	AC127462	AC127462 Danio rer
216	19	1.2	154895	2	AC020329	AC020329 Drosophil
c 217	19	1.2	156328	2	AC148280	AC148280 Sorex ara
c 218	19	1.2	157048	2	AC148303	AC148303 Sorex ara
c 219	19	1.2	157207	9	BX640542	BX640542 Human DNA
220	19	1.2	158536	2	CR339053	CR339053 Danio rer
c 221	19	1.2	158971	2	AP004882	AP004882 Oryza sat
222	19	1.2	159427	9	AL845454	AL845454 Human DNA
223	19	1.2	160333	2	AC145042	AC145042 Macropus
224	19	1.2	161406	9	AP002376	AP002376 Homo sapi
c 225	19	1.2	162556	9	AC006017	AC006017 Homo sapi
226	19	1.2	163025	14	AY372243	AY372243 Psittacid
c 227	19	1.2	163167	9	AC011347	AC011347 Homo sapi
228	19	1.2	163538	9	AC012598	AC012598 Homo sapi
c 229	19	1.2	163805	9	AC010956	AC010956 Homo sapi
230	19	1.2	164612	10	AC124697	AC124697 Mus muscu
231	19	1.2	166472	2	AC145009	AC145009 Bos tauru
232	19	1.2	167214	2	AC096202	AC096202 Rattus no
233	19	1.2	168997	2	AC021927	AC021927 Homo sapi
234	19	1.2	170167	10	AL672143	AL672143 Mouse DNA
c 235	19	1.2	170970	2	AC021564	AC021564 Homo sapi
c 236	19	1.2	171158	2	AC122983	AC122983 Rattus no
237	19	1.2	172157	2	AC125832	AC125832 Rattus no
238	19	1.2	172613	10	AL591953	AL591953 Mouse DNA

c 239	19	1.2	172637	6	AX686783	AX686783 Sequence
240	19	1.2	174656	2	AC019249	AC019249 Homo sapi
c 241	19	1.2	174710	2	AC069134	AC069134 Homo sapi
242	19	1.2	176362	2	AC149459	AC149459 Papio anu
243	19	1.2	176544	2	AL138877	AL138877 Homo sapi
244	19	1.2	176594	2	AC119325	AC119325 Rattus no
245	19	1.2	177251	10	AC124565	AC124565 Mus muscu
c 246	19	1.2	178730	9	AC148680	AC148680 Macaca mu
247	19	1.2	179712	2	AC135704	AC135704 Rattus no
c 248	19	1.2	180133	9	AL138885	AL138885 Human DNA
249	19	1.2	180816	2	AC110395	AC110395 Rattus no
250	19	1.2	180976	9	AL513321	AL513321 Human DNA
251	19	1.2	181955	3	AC008304	AC008304 Drosophil
c 252	19	1.2	183031	10	AC126795	AC126795 Mus muscu
253	19	1.2	183213	10	AL669952	AL669952 Mouse DNA
c 254	19	1.2	183338	2	AC083775	AC083775 Homo sapi
c 255	19	1.2	184021	3	AC093048	AC093048 Drosophil
c 256	19	1.2	184231	2	AC023651	AC023651 Homo sapi
257	19	1.2	185147	2	AC147193	AC147193 Papio anu
258	19	1.2	185560	2	AC129046	AC129046 Rattus no
c 259	19	1.2	186301	9	AL356962	AL356962 Human DNA
260	19	1.2	186380	5	BX004774	BX004774 Zebrafish
261	19	1.2	186437	9	AC146079	AC146079 Pan trogl
262	19	1.2	187088	10	AC133876	AC133876 Mus muscu
c 263	19	1.2	187718	2	AC112084	AC112084 Rattus no
c 264	19	1.2	188867	10	AC122012	AC122012 Mus muscu
265	19	1.2	188914	9	AC093744	AC093744 Homo sapi
266	19	1.2	189655	9	AC148670	AC148670 Macaca mu
c 267	19	1.2	189767	9	AL137145	AL137145 Human DNA
c 268	19	1.2	189840	9	AC012320	AC012320 Homo sapi
269	19	1.2	190182	2	AC149861	AC149861 Papio anu
c 270	19	1.2	191190	2	CR478286	CR478286 Danio rer
c 271	19	1.2	191300	2	AC109020	AC109020 Rattus no
272	19	1.2	191747	2	AC113675	AC113675 Rattus no
c 273	19	1.2	193639	2	AC127619	AC127619 Rattus no
c 274	19	1.2	194237	9	AC009063	AC009063 Homo sapi
275	19	1.2	194362	10	AC124716	AC124716 Mus muscu
276	19	1.2	195031	10	AL845265	AL845265 Mouse DNA
c 277	19	1.2	195057	2	BX897664	BX897664 Danio rer
278	19	1.2	195393	2	AC102703	AC102703 Mus muscu
c 279	19	1.2	196731	2	CR384092	CR384092 Danio rer
280	19	1.2	196788	2	AC021626	AC021626 Homo sapi
281	19	1.2	197170	2	AC133870	AC133870 Mus muscu
c 282	19	1.2	198400	2	AC138091	AC138091 Mus muscu
c 283	19	1.2	198638	2	AC139130	AC139130 Mus muscu
c 284	19	1.2	198794	9	AL583825	AL583825 Human DNA
c 285	19	1.2	198872	9	AF297093	AF297093 Homo sapi
c 286	19	1.2	199819	9	AC148682	AC148682 Macaca mu
287	19	1.2	201329	2	CR450778	CR450778 Danio rer
288	19	1.2	201620	10	AC131746	AC131746 Mus muscu
289	19	1.2	201862	2	AC150069	AC150069 Gallus ga
c 290	19	1.2	202237	10	AC114825	AC114825 Mus muscu
c 291	19	1.2	202515	9	AC148690	AC148690 Macaca mu
292	19	1.2	203700	2	AC141140	AC141140 Rattus no
c 293	19	1.2	204946	2	AC116145	AC116145 Mus muscu
c 294	19	1.2	205178	2	AC132020	AC132020 Rattus no
c 295	19	1.2	206538	2	AC111027	AC111027 Mus muscu
296	19	1.2	209337	2	AC122682	AC122682 Rattus no
c 297	19	1.2	209581	2	AC148275	AC148275 Papio anu
298	19	1.2	209772	9	AC099782	AC099782 Homo sapi
c 299	19	1.2	210616	2	BX324151	BX324151 Danio rer
300	19	1.2	211612	2	AC119144	AC119144 Rattus no
c 301	19	1.2	212475	2	AC093021	AC093021 Mus muscu
302	19	1.2	214121	2	AC141575	AC141575 Rattus no
c 303	19	1.2	216080	2	AC150049	AC150049 Gallus ga
c 304	19	1.2	216330	2	AC098443	AC098443 Rattus no
305	19	1.2	217711	10	AC116385	AC116385 Mus muscu
306	19	1.2	218267	9	AC148667	AC148667 Macaca mu
307	19	1.2	219553	2	HSA312687	AJ312687 Homo sapi
308	19	1.2	223717	2	AC108896	AC108896 Bos tauru
c 309	19	1.2	223827	2	AC079441	AC079441 Mus muscu
310	19	1.2	224219	2	AC115152	AC115152 Rattus no
311	19	1.2	224936	2	AC106537	AC106537 Rattus no
c 312	19	1.2	227595	2	CR450685	CR450685 Danio rer
c 313	19	1.2	228187	2	AC127107	AC127107 Rattus no
c 314	19	1.2	228202	5	BX284664	BX284664 Zebrafish
c 315	19	1.2	229540	2	AC132055	AC132055 Rattus no
c 316	19	1.2	230385	2	AC103227	AC103227 Rattus no
317	19	1.2	230611	2	AC126655	AC126655 Rattus no
318	19	1.2	231172	2	AC116887	AC116887 Mus muscu
c 319	19	1.2	233367	10	AC118931	AC118931 Mus muscu
c 320	19	1.2	234817	10	AL663048	AL663048 Mouse DNA
c 321	19	1.2	235024	2	AC120681	AC120681 Rattus no
c 322	19	1.2	235545	2	AC103084	AC103084 Rattus no
323	19	1.2	235668	2	AC110729	AC110729 Mus muscu
324	19	1.2	235681	2	AC150045	AC150045 Gallus ga
c 325	19	1.2	235700	2	AC103577	AC103577 Rattus no
326	19	1.2	235777	2	AC130900	AC130900 Rattus no
327	19	1.2	235814	2	AC106156	AC106156 Rattus no
328	19	1.2	237787	2	AC098758	AC098758 Rattus no
c 329	19	1.2	237961	6	AX504841	AX504841 Sequence
330	19	1.2	238365	2	AC107269	AC107269 Rattus no
331	19	1.2	238452	2	AC097019	AC097019 Rattus no
332	19	1.2	240181	2	AC098105	AC098105 Rattus no
c 333	19	1.2	241204	2	AC099185	AC099185 Rattus no
334	19	1.2	241420	2	AC094501	AC094501 Rattus no
335	19	1.2	241632	2	AC131461	AC131461 Rattus no
336	19	1.2	243073	2	AC108537	AC108537 Rattus no
337	19	1.2	247056	2	AC127765	AC127765 Rattus no
c 338	19	1.2	248390	2	AC118791	AC118791 Rattus no
c 339	19	1.2	248682	2	AC103093	AC103093 Rattus no
340	19	1.2	249900	2	AC097241	AC097241 Rattus no
341	19	1.2	250715	2	AC125673	AC125673 Rattus no
c 342	19	1.2	253693	2	AC093997	AC093997 Rattus no
343	19	1.2	256671	2	AC119533	AC119533 Rattus no
344	19	1.2	257572	2	AC125574	AC125574 Rattus no
c 345	19	1.2	262745	3	AE003658	AE003658 Drosophil
346	19	1.2	262917	2	AC097239	AC097239 Rattus no
c 347	19	1.2	263069	2	AC103440	AC103440 Rattus no
348	19	1.2	263319	2	AC125258	AC125258 Mus muscu
c 349	19	1.2	264095	9	AC008500	AC008500 Homo sapi
350	19	1.2	264232	2	CR626890	CR626890 Danio rer
351	19	1.2	264904	2	AC121259	AC121259 Mus muscu
c 352	19	1.2	267068	2	AC103090	AC103090 Rattus no
c 353	19	1.2	270098	2	AC097879	AC097879 Rattus no
c 354	19	1.2	272459	2	AC109059	AC109059 Rattus no
c 355	19	1.2	275060	2	AC135406	AC135406 Rattus no
c 356	19	1.2	276851	2	AC137860	AC137860 Mus muscu
c 357	19	1.2	277607	3	CEY105E8A	AL132876 Caenorhab
358	19	1.2	278375	2	AC130093	AC130093 Rattus no
c 359	19	1.2	279288	2	AC098526	AC098526 Rattus no
c 360	19	1.2	287955	2	AC095777	AC095777 Rattus no
c 361	19	1.2	288794	1	AE017279	AE017279 Bacillus
c 362	19	1.2	291804	1	AE017039	AE017039 Bacillus
c 363	19	1.2	293933	2	AC090040	AC090040 Homo sapi
364	19	1.2	298050	1	AP003129	AP003129 Staphyloc
365	19	1.2	299331	3	AE003460	AE003460 Drosophil
366	19	1.2	300235	2	AC123334	AC123334 Rattus no
367	19	1.2	300893	1	AE017006	AE017006 Bacillus
c 368	19	1.2	300902	2	AC111580	AC111580 Rattus no
c 369	19	1.2	300975	1	AE017013	AE017013 Bacillus
370	19	1.2	301903	1	AE016969	AE016969 Mycoplasm
c 371	19	1.2	301992	2	AC118360	AC118360 Rattus no
372	19	1.2	303396	2	AC092975	AC092975 Homo sapi
373	19	1.2	312227	2	AC120960	AC120960 Rattus no
c 374	19	1.2	314415	2	AC106697	AC106697 Rattus no
c 375	19	1.2	319486	9	AF055066	AF055066 Homo sapi
c 376	19	1.2	322058	2	AC068887	AC068887 Homo sapi
377	18	1.1	104	9	HSU32611	U32611 Human pre-B
378	18	1.1	125	6	AX900512	AX900512 Sequence
379	18	1.1	125	6	BD036045	BD036045 Sequence
380	18	1.1	153	6	AX907220	AX907220 Sequence
381	18	1.1	153	6	BD042753	BD042753 Sequence
c 382	18	1.1	167	9	AY488883S19	AY488901 Pan trogl
c 383	18	1.1	167	9	AY488911S19	AY488929 Gorilla g
c 384	18	1.1	167	9	AY488939S19	AY488957 Pongo pyg

c	385	18	1.1	167	9	AY488967S19 AY488985 Hylobates
	386	18	1.1	241	6	AR280863 AR280863 Sequence
	387	18	1.1	241	6	AR283359 AR283359 Sequence
	388	18	1.1	241	6	AR344127 AR344127 Sequence
	389	18	1.1	241	6	AR351328 AR351328 Sequence
	390	18	1.1	241	6	AR453908 AR453908 Sequence
	391	18	1.1	241	6	AX303051 AX303051 Sequence
c	392	18	1.1	273	11	G73222 G73222 Ppr106 fath
	393	18	1.1	300	6	BD219818 BD219818 Human gen
	394	18	1.1	334	8	FVE508252 AJ508252 Fragaria
	395	18	1.1	411	6	AX071678 AX071678 Sequence
c	396	18	1.1	444	5	AF369084 AF369084 Torpedo c
	397	18	1.1	451	6	BD275888 BD275888 COMPOUNDS
	398	18	1.1	451	6	AR220673 AR220673 Sequence
	399	18	1.1	451	6	AR255667 AR255667 Sequence
	400	18	1.1	451	6	AR281237 AR281237 Sequence
	401	18	1.1	451	6	AX365932 AX365932 Sequence
	402	18	1.1	458	6	AX156218 AX156218 Sequence
	403	18	1.1	484	5	AF376130 Danio rer AF376130 Danio rer
	404	18	1.1	489	6	AX911626 AX911626 Sequence
	405	18	1.1	489	6	BD047159 BD047159 Sequence
c	406	18	1.1	516	6	AX395894 AX395894 Sequence
c	407	18	1.1	525	6	CQ672104 CQ672104 Sequence
c	408	18	1.1	550	4	AB060696 AB060696 Bos tauru
c	409	18	1.1	575	3	AF526256 Chlamys f AF526256 Chlamys f
	410	18	1.1	578	6	CQ522113 CQ522113 Sequence
	411	18	1.1	600	9	HSW30CF X16414 Human DNA f
	412	18	1.1	600	11	G19996 G19996 sWSS858 Eri
	413	18	1.1	627	11	BV031831 BV031831 S212P6435
	414	18	1.1	631	8	AF320290 AF320290 Secale mo
c	415	18	1.1	634	11	BV068201 BV068201 S212P6227
c	416	18	1.1	648	11	G77415 G77415 S208P6117FC
c	417	18	1.1	779	3	AY617223 AY617223 Sterkiell
	418	18	1.1	792	6	AX412851 AX412851 Sequence
	419	18	1.1	792	6	AX506560 AX506560 Sequence
	420	18	1.1	792	6	AX652052 AX652052 Sequence
	421	18	1.1	792	8	AY097422 AY097422 Arabidops
	422	18	1.1	895	8	AF446363 AF446363 Arabidops
c	423	18	1.1	912	6	A47120 A47120 Sequence 1
c	424	18	1.1	912	6	CQ812252 CQ812252 Sequence
	425	18	1.1	912	8	AY088521 AY088521 Arabidops
c	426	18	1.1	912	9	HSBTF2P35 Z30093 H.sapiens m
	427	18	1.1	932	5	BX950461 BX950461 Gallus ga
c	428	18	1.1	1024	6	AX790555 AX790555 Sequence
c	429	18	1.1	1029	9	BC065250 BC065250 Homo sapi
c	430	18	1.1	1232	6	AR339181 AR339181 Sequence
c	431	18	1.1	1236	9	BC031030 BC031030 Homo sapi
	432	18	1.1	1339	5	GGCBPAMR X64539 G.domesticu
	433	18	1.1	1360	5	BC056300 BC056300 Danio rer
	434	18	1.1	1363	5	BC065991 BC065991 Danio rer
c	435	18	1.1	1460	9	BC047868 BC047868 Homo sapi
c	436	18	1.1	1539	6	AX066377 AX066377 Sequence
c	437	18	1.1	1543	6	BD092607 BD092607 Identific
c	438	18	1.1	1548	9	BC039857 BC039857 Homo sapi
c	439	18	1.1	1554	6	AX121665 AX121665 Sequence
c	440	18	1.1	1554	6	BD163782 BD163782 Novel pol
c	441	18	1.1	1603	6	AX756597 AX756597 Sequence
c	442	18	1.1	1634	10	AF314820 AF314820 Rattus no
	443	18	1.1	1743	9	AB089319 AB089319 Homo sapi
	444	18	1.1	1747	6	BD136405 BD136405 95 human
	445	18	1.1	1748	6	AX827805 AX827805 Sequence
	446	18	1.1	1748	10	RNU72349 U72349 Rattus norv
	447	18	1.1	1774	10	MMNORRIE X92397 M.musculus
c	448	18	1.1	2069	10	D45208 D45208 Mus musculu
c	449	18	1.1	2105	10	BC047133 BC047133 Mus muscu
	450	18	1.1	2214	14	AY530556 AY530556 Adeno-ass
	451	18	1.1	2304	6	AX544437 AX544437 Sequence
c	452	18	1.1	2334	9	BC039726 BC039726 Homo sapi
c	453	18	1.1	2336	9	BC040439 BC040439 Homo sapi
	454	18	1.1	2375	10	AY141038 AY141038 Rattus no
c	455	18	1.1	2414	6	AX876687 AX876687 Sequence
c	456	18	1.1	2414	6	BD156262 BD156262 Primer fo
c	457	18	1.1	2414	9	AK001411 AK001411 Homo sapi
c	458	18	1.1	2475	8	AK068162 AK068162 Oryza sat
	459	18	1.1	2509	6	AX078700 AX078700 Sequence
c	460	18	1.1	2629	10	AF136751 AF136751 Mus muscu
c	461	18	1.1	2673	8	AB032074 AB032074 Nicotiana
c	462	18	1.1	2701	6	E26903 E26903 Novel potas
c	463	18	1.1	2827	8	AK103089 AK103089 Oryza sat
c	464	18	1.1	2827	8	AK110496 AK110496 Oryza sat
c	465	18	1.1	2855	10	AF337809 AF337809 Rattus no
c	466	18	1.1	3078	8	KLU40151 U40151 Kluyveromyc
	467	18	1.1	3149	6	CQ834736 CQ834736 Sequence
	468	18	1.1	3149	6	CQ834738 CQ834738 Sequence
	469	18	1.1	3190	9	AB056846 AB056846 Macaca fa
	470	18	1.1	3190	9	AB056847 AB056847 Macaca fa
	471	18	1.1	3268	9	HSGPIP137 Z48042 H.sapiens m
c	472	18	1.1	3278	6	I32736 I32736 Sequence 13
c	473	18	1.1	3278	6	I38712 I38712 Sequence 13
	474	18	1.1	3352	9	HSM805773 BX537699 Homo sapi
c	475	18	1.1	3380	8	AY566621 AY566621 Acer circ
	476	18	1.1	3477	9	BC001731 BC001731 Homo sapi
	477	18	1.1	3521	6	BD235119 BD235119 Human MP5
	478	18	1.1	3521	6	E31260 E31260 Human MP52
	479	18	1.1	3522	9	AB019005 AB019005 Homo sapi
	480	18	1.1	3582	6	AX751713 AX751713 Sequence
c	481	18	1.1	3760	9	BC034607 BC034607 Homo sapi
c	482	18	1.1	3859	2	AC015166 AC015166 Drosophil
c	483	18	1.1	3887	6	AX876625 AX876625 Sequence
c	484	18	1.1	3887	6	BD156228 BD156228 Primer fo
c	485	18	1.1	3887	9	AK001379 AK001379 Homo sapi
	486	18	1.1	4060	10	BC011271 BC011271 Mus muscu
	487	18	1.1	4385	6	AX753250 AX753250 Sequence
c	488	18	1.1	4470	9	HSA223948 AJ223948 Homo sapi
	489	18	1.1	4586	6	AR339039 AR339039 Sequence
	490	18	1.1	4662	3	CEY102A5B AL023821 Caenorhab
	491	18	1.1	4684	10	AB029482 AB029482 Mus muscu
c	492	18	1.1	4931	6	CQ716621 CQ716621 Sequence
c	493	18	1.1	5143	5	BC072296 BC072296 Xenopus l
c	494	18	1.1	5329	3	DMUQ80FP X69119 D.melanogas
	495	18	1.1	5359	9	AF338357 AF338357 Pan trogl
c	496	18	1.1	5473	6	AR338769 AR338769 Sequence
c	497	18	1.1	5760	9	HSM808955 BX648804 Homo sapi
	498	18	1.1	5924	8	MM4DTD Z73640 Mucor muced
	499	18	1.1	6035	9	HSM808873 BX648722 Homo sapi
	500	18	1.1	6222	10	AK122323 AK122323 Mus muscu
c	501	18	1.1	6382	1	AY550111 AY550111 Bacillus
c	502	18	1.1	6412	6	CQ598409 CQ598409 Sequence
c	503	18	1.1	6450	9	AY013288 AY013288 Homo sapi
	504	18	1.1	6943	10	BC070449 BC070449 Mus muscu
c	505	18	1.1	7315	9	HSM805565 AL834463 Homo sapi
	506	18	1.1	7650	9	HSM806134 BX537997 Homo sapi
	507	18	1.1	10029	1	AE006872 AE006872 Sulfolobu
	508	18	1.1	10157	6	CQ724045 CQ724045 Sequence
	509	18	1.1	10172	6	AX333220 AX333220 Sequence
	510	18	1.1	10172	9	HSU03272 U03272 Human fibri
c	511	18	1.1	10371	9	AY508451 AY508451 Gorilla g
c	512	18	1.1	10416	9	AY367067 AY367067 Pongo pyg
c	513	18	1.1	10422	9	AY485422 AY485422 Aotus sp.
c	514	18	1.1	10428	9	AY486114 AY486114 Cercopith
c	515	18	1.1	10431	9	AY485418 AY485418 Macaca fa
c	516	18	1.1	10434	9	AF509326 AF509326 Homo sapi
c	517	18	1.1	10434	9	AY367065 AY367065 Homo sapi
c	518	18	1.1	10434	9	AY367066 AY367066 Pan trogl
c	519	18	1.1	10434	9	AY508452 AY508452 Pan trogl
c	520	18	1.1	12019	1	AE011442 AE011442 Leptospir
c	521	18	1.1	12186	1	AE000577 AE000577 Helicobac
	522	18	1.1	13114	1	AE010650 AE010650 Fusobacte
c	523	18	1.1	14203	1	AE000948 AE000948 Archaeogl
c	524	18	1.1	16383	4	CMA554052 AJ554052 Caperea m
c	525	18	1.1	16390	4	BMY554051 AJ554051 Balaena m
c	526	18	1.1	16398	4	MIBPCG X61145 Balaenopter
c	527	18	1.1	16402	4	MIBMCG X72204 Balaenopter
c	528	18	1.1	16412	4	ERO554053 AJ554053 Eschricht
c	529	18	1.1	16829	4	RUMTGENOM X97336 Rhinoceros
c	530	18	1.1	16832	4	MTCSXX Y07726 Ceratotheri

c 531	18	1.1	17734	4	LEU421471	AJ421471 Lepus eur
532	18	1.1	18954	9	AY339617	AY339617 Homo sapi
c 533	18	1.1	28842	9	AL160158	AL160158 Human DNA
c 534	18	1.1	30788	3	AC078892	AC078892 Leishmani
c 535	18	1.1	31930	9	U73331	U73331 Homo sapien
c 536	18	1.1	32202	3	U00050	U00050 Caenorhabdi
537	18	1.1	32987	1	AB036666	AB036666 Wolbachia
538	18	1.1	33579	2	AC149419	AC149419 Phakopsor
539	18	1.1	34518	9	AC107083	AC107083 Homo sapi
c 540	18	1.1	34518	9	AC107083	AC107083 Homo sapi
541	18	1.1	34796	5	BX005325	BX005325 Zebrafish
c 542	18	1.1	35899	2	AC149378	AC149378 Phakopsor
c 543	18	1.1	36524	7	AF157835	AF157835 Bacteriop
544	18	1.1	37129	2	AC149360	AC149360 Phakopsor
545	18	1.1	37702	9	AP001234	AP001234 Homo sapi
c 546	18	1.1	38013	9	HSL17A9B	Z54335 Human DNA s
c 547	18	1.1	38881	2	AC149371	AC149371 Phakopsor
c 548	18	1.1	38932	9	HSN38E12	Z68287 Human DNA s
549	18	1.1	39104	6	AX059483	AX059483 Sequence
c 550	18	1.1	40081	2	AC145669	AC145669 Homo sapi
c 551	18	1.1	40302	3	CEC11G6	Z70204 Caenorhabdi
c 552	18	1.1	41147	2	AC149423	AC149423 Phakopsor
c 553	18	1.1	41308	9	AC004196	AC004196 Homo sapi
c 554	18	1.1	43722	2	AC141451	AC141451 Homo sapi
555	18	1.1	44548	9	AF020801	AF020801 Homo sapi
556	18	1.1	44577	6	AX695929	AX695929 Sequence
557	18	1.1	48000	2	AC020147	AC020147 Drosophil
558	18	1.1	50487	2	AC068211	AC068211 Homo sapi
c 559	18	1.1	52207	2	AC019584	AC019584 Drosophil
c 560	18	1.1	52358	9	HS27C10	AL031803 Human DNA
561	18	1.1	54456	9	AL591047	AL591047 Human DNA
c 562	18	1.1	55219	2	AC100542	AC100542 Mus muscu
c 563	18	1.1	58155	2	AC100949	AC100949 Mus muscu
c 564	18	1.1	58179	2	AC090272	AC090272 Homo sapi
c 565	18	1.1	58536	9	AL161718	AL161718 Human DNA
566	18	1.1	59012	9	HSABLGR2	U07562 Human ABL g
c 567	18	1.1	59932	2	AC101471	AC101471 Mus muscu
568	18	1.1	61946	9	AF020802	AF020802 Homo sapi
c 569	18	1.1	62370	2	AL451008	AL451008 Homo sapi
570	18	1.1	62377	2	AL360009	AL360009 Homo sapi
571	18	1.1	62544	2	AY339212	AY339212 Takifugu
572	18	1.1	63090	9	AC087320	AC087320 Homo sapi
573	18	1.1	63633	9	AL139409	AL139409 Human DNA
574	18	1.1	63894	2	AC140885_3	Continuation (4 of
575	18	1.1	64703	2	AC136718	AC136718 Homo sapi
c 576	18	1.1	65389	9	AY497017	AY497017 Pongo pyg
c 577	18	1.1	65600	9	AY497013	AY497013 Macaca mu
c 578	18	1.1	66069	9	AY497016	AY497016 Pan trogl
c 579	18	1.1	66089	9	AY497014	AY497014 Gorilla g
c 580	18	1.1	68332	2	AC107155_3	Continuation (4 of
c 581	18	1.1	68554	2	AC010416	AC010416 Homo sapi
582	18	1.1	68589	2	AC087682	AC087682 Homo sapi
583	18	1.1	68986	8	T22I11	AC012190 Arabidops
584	18	1.1	69017	9	HS410I8	AL031732 Human DNA
c 585	18	1.1	69093	2	AC134785	AC134785 Homo sapi
c 586	18	1.1	69731	2	AC116014	AC116014 Homo sapi
c 587	18	1.1	69745	9	AC114801	AC114801 Homo sapi
588	18	1.1	70642	2	AC099870	AC099870 Mus muscu
589	18	1.1	71091	9	AC106052	AC106052 Homo sapi
c 590	18	1.1	71179	9	AL136110	AL136110 Human DNA
591	18	1.1	71927	2	AC024464	AC024464 Homo sapi
c 592	18	1.1	73218	9	HS209H1	Z84465 Human DNA s
593	18	1.1	75621	9	BX247900	BX247900 Human DNA
c 594	18	1.1	75688	5	AC149073	AC149073 Sequence
595	18	1.1	75709	8	AB010693	AB010693 Arabidops
596	18	1.1	76581	9	AL355304	AL355304 Human DNA
597	18	1.1	77858	2	AC135758	AC135758 Rattus no
598	18	1.1	80662	9	AL645929	AL645929 Human DNA
599	18	1.1	81188	2	AP001128	AP001128 Homo sapi
600	18	1.1	81780	9	AL161440	AL161440 Human DNA
c 601	18	1.1	82359	8	ATAC002342	AC002342 Arabidops
c 602	18	1.1	82422	9	AL138763	AL138763 Human DNA
603	18	1.1	82599	8	AP004498	AP004498 Lotus cor
604	18	1.1	82646	8	AB028611	AB028611 Arabidops
605	18	1.1	82944	9	AL354999	AL354999 Human DNA
c 606	18	1.1	84553	4	AC123538	AC123538 Sminthops
c 607	18	1.1	84649	2	AC013534	AC013534 Homo sapi
608	18	1.1	85801	9	AL805909	AL805909 Human DNA
609	18	1.1	85848	2	AC015733	AC015733 Homo sapi
610	18	1.1	86005	2	AC021938	AC021938 Homo sapi
c 611	18	1.1	86377	8	ATF17N18	AL049751 Arabidops
612	18	1.1	86630	9	AL592428	AL592428 Human DNA
c 613	18	1.1	86764	10	BX842611	BX842611 Mouse DNA
c 614	18	1.1	87575	8	AC011622	AC011622 Arabidops
c 615	18	1.1	87768	8	T22H22	AC005388 Sequence
616	18	1.1	88251	2	AC126325	AC126325 Homo sapi
c 617	18	1.1	88823	9	AL713965	AL713965 Human DNA
618	18	1.1	89177	9	AL356000	AL356000 Human DNA
619	18	1.1	89203	2	AC119504	AC119504 Rattus no
c 620	18	1.1	90011	9	AL360007	AL360007 Human DNA
c 621	18	1.1	90034	9	AP002012	AP002012 Homo sapi
622	18	1.1	90525	5	BX510955	BX510955 Zebrafish
c 623	18	1.1	96066	8	AC005662	AC005662 Arabidops
624	18	1.1	97095	2	AC141824	AC141824 Apis mell
c 625	18	1.1	97142	2	AC010439	AC010439 Homo sapi
c 626	18	1.1	98800	10	BX510362	BX510362 Mouse DNA
c 627	18	1.1	99416	9	AC105276	AC105276 Homo sapi
c 628	18	1.1	99999	9	AP000510	AP000510 Homo sapi
c 629	18	1.1	100382	9	AL162292	AL162292 Human DNA
c 630	18	1.1	102425	9	AC011363	AC011363 Homo sapi
c 631	18	1.1	102714	9	AP000692	AP000692 Homo sapi
c 632	18	1.1	102757	9	AL353698	AL353698 Human DNA
c 633	18	1.1	102992	2	AL591863	AL591863 Homo sapi
634	18	1.1	103428	2	AC096436_6	Continuation (7 of
635	18	1.1	103950	9	AC034235	AC034235 Homo sapi
636	18	1.1	104228	9	AL135917	AL135917 Human DNA
637	18	1.1	104485	10	AB114903	AB114903 Mus muscu
c 638	18	1.1	105499	9	AC093335	AC093335 Homo sapi
639	18	1.1	106159	4	AC124041	AC124041 Oryctolag
c 640	18	1.1	106248	5	AL929595	AL929595 Zebrafish
c 641	18	1.1	108175	9	AC068206	AC068206 Homo sapi
642	18	1.1	108661	9	AC034214	AC034214 Homo sapi
c 643	18	1.1	108700	9	AC131952	AC131952 Homo sapi
c 644	18	1.1	109296	9	AC083949	AC083949 Homo sapi
c 645	18	1.1	109439	2	AC019325	AC019325 Homo sapi
646	18	1.1	110000	1	AE000516_02	Continuation (3 of
c 647	18	1.1	110000	1	BX908798_06	Continuation (7 of
c 648	18	1.1	110000	2	AC108442_0	AC108442 Mus muscu
649	18	1.1	110000	2	AC114782_0	AC114782 Homo sapi
650	18	1.1	110000	2	AC114782_1	Continuation (2 of
c 651	18	1.1	110000	2	AC119593_2	Continuation (3 of
c 652	18	1.1	110000	2	AC120236_2	Continuation (3 of
653	18	1.1	110000	2	AC128782_3	Continuation (4 of
c 654	18	1.1	110000	2	AC129424_2	Continuation (3 of
c 655	18	1.1	110000	2	AC132794_4	Continuation (5 of
c 656	18	1.1	110000	2	AC141459_0	AC141459 Homo sapi
c 657	18	1.1	110000	2	AC142960_0	AC142960 Macaca mu
658	18	1.1	110000	2	AP006490_3	Continuation (4 of
c 659	18	1.1	110000	2	PFMAL7P1_06	Continuation (7 of
660	18	1.1	110000	8	CR380951_5	Continuation (6 of
c 661	18	1.1	110000	8	CR382122_04	Continuation (5 of
c 662	18	1.1	110000	8	CR382123_14	Continuation (15 o
c 663	18	1.1	110391	10	AF390547	AF390547 Mus muscu
c 664	18	1.1	110494	8	AP004139	AP004139 Oryza sat
c 665	18	1.1	112182	2	AC141177	AC141177 Rattus no
c 666	18	1.1	112268	8	AC093490	AC093490 Oryza sat
c 667	18	1.1	112560	9	HSJ513G18	AL109760 Human DNA
c 668	18	1.1	112626	9	AC093748	AC093748 Homo sapi
c 669	18	1.1	113214	2	AC011344	AC011344 Homo sapi
670	18	1.1	113332	8	CNS08C7Z	AL731750 Oryza sat
c 671	18	1.1	113415	2	AP004860	AP004860 Oryza sat
672	18	1.1	114127	9	AC008683	AC008683 Homo sapi
c 673	18	1.1	114688	9	AC125437	AC125437 Homo sapi
674	18	1.1	114691	4	AC144636	AC144636 Artibeus
675	18	1.1	115224	9	AL356234	AL356234 Human DNA
c 676	18	1.1	115890	10	AC114412	AC114412 Mus muscu

	677	18	1.1 116098	2	AC023867	AC023867 Homo sapi
c	678	18	1.1 117084	9	AL139247	AL139247 Human DNA
	679	18	1.1 117327	9	AL663093	AL663093 Human DNA
	680	18	1.1 117714	3	AC098797	AC098797 Leishmani
	681	18	1.1 119307	9	AC004134	AC004134 Homo sapi
c	682	18	1.1 119525	8	AP006366	AP006366 Lotus cor
c	683	18	1.1 119944	9	AC111162	AC111162 Homo sapi
	684	18	1.1 120405	2	AC046147	AC046147 Mus muscu
	685	18	1.1 120594	2	AC149264	AC149264 Medicago
	686	18	1.1 121207	8	AP006077	AP006077 Lotus cor
c	687	18	1.1 122842	2	AC129474	AC129474 Homo sapi
	688	18	1.1 123369	9	AC025170	AC025170 Homo sapi
	689	18	1.1 124329	2	AC144420	AC144420 Rattus no
	690	18	1.1 124661	2	AC127541	AC127541 Homo sapi
c	691	18	1.1 125304	9	AC008044	AC008044 Homo sapi
	692	18	1.1 125502	8	ATT4L20	AL023094 Arabidops
	693	18	1.1 126222	2	AL844492	AL844492 Homo sapi
	694	18	1.1 126394	9	AC109998	AC109998 Homo sapi
	695	18	1.1 127526	9	AC006315	AC006315 Homo sapi
	696	18	1.1 129109	9	AL390239	AL390239 Human DNA
c	697	18	1.1 129257	2	AC148368	AC148368 Meleagris
	698	18	1.1 129361	9	AL603789	AL603789 Human DNA
c	699	18	1.1 129782	5	BX120005	BX120005 Zebrafish
	700	18	1.1 129880	9	AC104334	AC104334 Homo sapi
c	701	18	1.1 130307	9	AC113355	AC113355 Homo sapi
c	702	18	1.1 130870	10	AL731775	AL731775 Mouse DNA
	703	18	1.1 131312	9	AC008456	AC008456 Homo sapi
c	704	18	1.1 131387	10	AC079440	AC079440 Mus muscu
c	705	18	1.1 131489	9	AC093505	AC093505 Homo sapi
c	706	18	1.1 131637	9	CNS01DUC	AL133239 Human chr
c	707	18	1.1 131743	8	AC004561	AC004561 Arabidops
	708	18	1.1 132191	9	AC090349	AC090349 Homo sapi
	709	18	1.1 132301	2	AC129954	AC129954 Bos tauru
	710	18	1.1 132492	9	AC007616	AC007616 Homo sapi
	711	18	1.1 132585	9	AC131947	AC131947 Homo sapi
c	712	18	1.1 132647	8	AC073393	AC073393 Oryza sat
c	713	18	1.1 132867	9	AC004601	AC004601 Human 11p
	714	18	1.1 132953	9	AC003015	AC003015 Human BAC
	715	18	1.1 133028	8	AP003447	AP003447 Oryza sat
c	716	18	1.1 133563	2	AC099481	AC099481 Homo sapi
	717	18	1.1 133843	8	AC003981	AC003981 Genomic s
c	718	18	1.1 133910	10	AL929253	AL929253 Mouse DNA
	719	18	1.1 134369	9	AC104825	AC104825 Homo sapi
c	720	18	1.1 135079	9	HSDJ70A9	AL121788 Human DNA
	721	18	1.1 135396	9	BX927139	BX927139 Human DNA
c	722	18	1.1 135505	9	AC004477	AC004477 Homo sapi
	723	18	1.1 135545	10	MMHC213L3	AF109905 Mus muscu
c	724	18	1.1 135726	8	AC147498	AC147498 Medicago
	725	18	1.1 136544	9	AC127033	AC127033 Homo sapi
c	726	18	1.1 137554	2	AC127618	AC127618 Rattus no
	727	18	1.1 137557	9	AC005909	AC005909 Homo sapi
	728	18	1.1 138041	9	CNS01DUI	AL133245 BAC seque
	729	18	1.1 138586	8	AC144726	AC144726 Medicago
	730	18	1.1 138909	9	CNS01DS3	AL121653 BAC seque
	731	18	1.1 138951	2	AC115068	AC115068 Mus muscu
c	732	18	1.1 139444	9	HS380C13	AL022161 Human DNA
c	733	18	1.1 139469	2	AC143350	AC143350 Homo sapi
c	734	18	1.1 139512	9	HSJ1169J3	AL049652 Human DNA
c	735	18	1.1 139558	10	AL929129	AL929129 Mouse DNA
c	736	18	1.1 139653	2	AP005890	AP005890 Oryza sat
c	737	18	1.1 139796	8	AP005782	AP005782 Oryza sat
c	738	18	1.1 141073	9	AC105108	AC105108 Homo sapi
c	739	18	1.1 141275	8	AP003141	AP003141 Oryza sat
	740	18	1.1 141368	8	AC134341	AC134341 Oryza sat
c	741	18	1.1 141401	10	AL844585	AL844585 Mouse DNA
c	742	18	1.1 141447	9	AC016204	AC016204 Homo sapi
	743	18	1.1 141767	9	BS000199	BS000199 Pan trogl
	744	18	1.1 141772	2	BX571792	BX571792 Danio rer
	745	18	1.1 141855	2	AC103905	AC103905 Canis fam
c	746	18	1.1 142234	9	AC110620	AC110620 Homo sapi
	747	18	1.1 142649	10	AC134847	AC134847 Mus muscu
	748	18	1.1 142659	8	AP003520	AP003520 Oryza sat
c	749	18	1.1 142956	8	AP004641	AP004641 Oryza sat
c	750	18	1.1 143088	9	AC005684	AC005684 Homo sapi
	751	18	1.1 143841	9	AC008964	AC008964 Homo sapi
	752	18	1.1 144116	10	AL671907	AL671907 Mouse DNA
c	753	18	1.1 144136	2	AC012243	AC012243 Homo sapi
c	754	18	1.1 144234	2	AP002425	AP002425 Homo sapi
	755	18	1.1 144279	2	AP001570	AP001570 Homo sapi
c	756	18	1.1 144348	2	AC016423	AC016423 Homo sapi
c	757	18	1.1 144709	2	AC120084	AC120084 Rattus no
c	758	18	1.1 144924	9	HSDJ697P8	AL050403 Human DNA
c	759	18	1.1 144941	9	AL591848	AL591848 Human DNA
c	760	18	1.1 145270	10	AC140366	AC140366 Mus muscu
	761	18	1.1 145383	2	AC116816	AC116816 Mus muscu
c	762	18	1.1 145859	9	AC116336	AC116336 Homo sapi
	763	18	1.1 146154	2	AP004400	AP004400 Oryza sat
c	764	18	1.1 146366	9	AL627231	AL627231 Human DNA
	765	18	1.1 146671	9	AC093810	AC093810 Homo sapi
	766	18	1.1 146691	2	AP002402	AP002402 Homo sapi
	767	18	1.1 146916	2	AC026931	AC026931 Homo sapi
	768	18	1.1 147109	9	AL591043	AL591043 Human DNA
	769	18	1.1 147367	2	AC073966	AC073966 Homo sapi
c	770	18	1.1 147367	2	AC073966	AC073966 Homo sapi
c	771	18	1.1 147859	9	AC092993	AC092993 Homo sapi
	772	18	1.1 147940	2	AC026913	AC026913 Homo sapi
	773	18	1.1 148345	9	AL592151	AL592151 Human DNA
c	774	18	1.1 148491	8	AP005929	AP005929 Oryza sat
c	775	18	1.1 149453	10	AC084109	AC084109 Mus muscu
	776	18	1.1 150021	5	BX088691	BX088691 Zebrafish
c	777	18	1.1 150145	9	AC069216	AC069216 Homo sapi
	778	18	1.1 150159	2	AC018791	AC018791 Homo sapi
	779	18	1.1 150399	2	AC009369	AC009369 Drosophil
	780	18	1.1 150565	2	BX927078	BX927078 Danio rer
c	781	18	1.1 150680	9	AC090894	AC090894 Homo sapi
	782	18	1.1 150817	2	AC021762	AC021762 Homo sapi
c	783	18	1.1 150879	2	AC074017	AC074017 Homo sapi
c	784	18	1.1 151235	9	AC090936	AC090936 Homo sapi
c	785	18	1.1 151325	9	AC074363	AC074363 Homo sapi
	786	18	1.1 151446	5	AL627088	AL627088 Zebrafish
	787	18	1.1 151708	2	AL929460	AL929460 Danio rer
	788	18	1.1 151784	2	AC138664	AC138664 Mus muscu
	789	18	1.1 151828	8	AC018632	AC018632 Genomic S
c	790	18	1.1 151847	2	AC022792	AC022792 Homo sapi
c	791	18	1.1 151923	10	AL845499	AL845499 Mouse DNA
c	792	18	1.1 152181	9	AL391869	AL391869 Human DNA
	793	18	1.1 152336	9	AP004714	AP004714 Homo sapi
	794	18	1.1 152787	2	AC026623	AC026623 Homo sapi
	795	18	1.1 153064	8	CNS08CAL	AL831808 Oryza sat
	796	18	1.1 153096	2	AC022044	AC022044 Homo sapi
	797	18	1.1 153295	2	AC060758	AC060758 Homo sapi
	798	18	1.1 153365	2	AC142443	AC142443 Homo sapi
c	799	18	1.1 153605	2	AC147764	AC147764 Dasypus n
c	800	18	1.1 153743	8	AP005108	AP005108 Oryza sat
c	801	18	1.1 153897	5	AL928656	AL928656 Zebrafish
	802	18	1.1 154085	2	BX537124	BX537124 Danio rer
c	803	18	1.1 154285	9	AL606923	AL606923 Human DNA
c	804	18	1.1 154315	9	AP005380	AP005380 Homo sapi
	805	18	1.1 154594	9	AL161722	AL161722 Human DNA
c	806	18	1.1 154665	2	AC144355	AC144355 Homo sapi
c	807	18	1.1 154713	9	AC013361	AC013361 Homo sapi
	808	18	1.1 155198	2	AL357553	AL357553 Homo sapi
	809	18	1.1 155379	9	HS616B8	AL023803 Human DNA
	810	18	1.1 155413	9	AC068304	AC068304 Homo sapi
c	811	18	1.1 155613	2	AC149867	AC149867 Papio anu
c	812	18	1.1 155868	9	AC016764	AC016764 Homo sapi
	813	18	1.1 155892	9	AL353809	AL353809 Human DNA
c	814	18	1.1 156193	10	AL669907	AL669907 Mouse DNA
	815	18	1.1 156272	9	AL669830	AL669830 Human DNA
c	816	18	1.1 156432	9	HS581F7	AL022164 Human DNA
	817	18	1.1 156513	9	AC140770	AC140770 Homo sapi
c	818	18	1.1 156540	2	CR376786	CR376786 Danio rer
c	819	18	1.1 157042	9	AC024061	AC024061 Homo sapi
c	820	18	1.1 157054	2	AC021782	AC021782 Homo sapi
c	821	18	1.1 157197	2	AC134636	AC134636 Rattus no
c	822	18	1.1 157321	9	AC068811	AC068811 Homo sapi

	823	18	1.1	157402	2	AC034161 AC034161 Homo sapi
c	824	18	1.1	157410	2	AC143922 AC143922 Macaca mu
c	825	18	1.1	157592	2	AC145798 AC145798 Xenopus t
c	826	18	1.1	158072	2	AC053533 AC053533 Homo sapi
	827	18	1.1	158168	2	AC142544 AC142544 Homo sapi
	828	18	1.1	158180	9	AC100781 AC100781 Homo sapi
	829	18	1.1	158224	5	BX323886 BX323886 Zebrafish
c	830	18	1.1	158229	2	AC133596 AC133596 Homo sapi
c	831	18	1.1	158508	9	AC107622 AC107622 Homo sapi
c	832	18	1.1	158595	9	AC010614 AC010614 Homo sapi
	833	18	1.1	158785	2	AC027699 AC027699 Homo sapi
	834	18	1.1	158816	3	AC009368 AC009368 Drosophil
c	835	18	1.1	159128	10	AL928557 AL928557 Mouse DNA
	836	18	1.1	159322	2	BX957240 BX957240 Danio rer
	837	18	1.1	159480	9	AC021843 AC021843 Homo sapi
c	838	18	1.1	159577	2	AC080060 AC080060 Homo sapi
c	839	18	1.1	159723	2	AC021862 AC021862 Homo sapi
	840	18	1.1	160379	5	BX323558 BX323558 Zebrafish
	841	18	1.1	160390	2	AC129676 AC129676 Homo sapi
	842	18	1.1	160472	2	AC080140 AC080140 Mus muscu
c	843	18	1.1	160583	2	AC010968 AC010968 Homo sapi
c	844	18	1.1	160869	2	AC026378 AC026378 Mus muscu
	845	18	1.1	160918	2	AC069196 AC069196 Homo sapi
c	846	18	1.1	161136	2	AC142078 AC142078 Homo sapi
	847	18	1.1	161653	2	AC026619 AC026619 Homo sapi
c	848	18	1.1	161672	2	AC136667 AC136667 Rattus no
	849	18	1.1	161685	2	AC103901 AC103901 Canis fam
c	850	18	1.1	161754	3	AC007451 AC007451 Drosophil
c	851	18	1.1	161865	8	AP005912 AP005912 Oryza sat
c	852	18	1.1	161883	2	AC025825 AC025825 Oryza sat
c	853	18	1.1	161920	9	AC025169 AC025169 Homo sapi
c	854	18	1.1	162088	2	AC069479 AC069479 Homo sapi
c	855	18	1.1	162115	5	BX569788 BX569788 Zebrafish
	856	18	1.1	162150	9	AC093877 AC093877 Homo sapi
c	857	18	1.1	162352	2	AC150523 AC150523 Bos tauru
c	858	18	1.1	162355	2	AC126015 AC126015 Medicago
	859	18	1.1	162489	9	AP001572 AP001572 Homo sapi
c	860	18	1.1	162522	2	AC021014 AC021014 Homo sapi
	861	18	1.1	162691	2	AC013523 AC013523 Homo sapi
c	862	18	1.1	162784	9	AC011197 AC011197 Homo sapi
	863	18	1.1	162881	9	AC022174 AC022174 Homo sapi
	864	18	1.1	162964	9	AC011939 AC011939 Homo sapi
c	865	18	1.1	163050	2	AC020696 AC020696 Homo sapi
	866	18	1.1	163316	9	AL161420 AL161420 Human DNA
	867	18	1.1	163373	2	AC024263 AC024263 Homo sapi
c	868	18	1.1	163389	9	AL589765 AL589765 Human DNA
	869	18	1.1	163419	5	BX323847 BX323847 Zebrafish
	870	18	1.1	163776	2	AC109289 AC109289 Mus muscu
	871	18	1.1	163788	2	AC018996 AC018996 Homo sapi
c	872	18	1.1	164018	9	AL354868 AL354868 Human DNA
c	873	18	1.1	164219	5	BX005205 BX005205 Zebrafish
c	874	18	1.1	164454	9	AC093431 AC093431 Homo sapi
c	875	18	1.1	164514	9	CNS01RGV AL160211 Human chr
	876	18	1.1	164567	8	OSJN00072 AL606639 Oryza sat
c	877	18	1.1	164589	2	AC026043 AC026043 Homo sapi
c	878	18	1.1	164611	2	AC128858 AC128858 Rattus no
c	879	18	1.1	164630	2	AC136099 AC136099 Rattus no
c	880	18	1.1	164656	2	AC149122 AC149122 Papio anu
c	881	18	1.1	164733	2	AC117341 AC117341 Rattus no
c	882	18	1.1	164798	9	AC092598 AC092598 Homo sapi
	883	18	1.1	164820	9	AL627443 AL627443 Human DNA
c	884	18	1.1	164823	9	AC009567 AC009567 Homo sapi
	885	18	1.1	165072	9	AC148684 AC148684 Macaca mu
	886	18	1.1	165168	2	AC148167 AC148167 Zea mays
	887	18	1.1	165287	9	AC090599 AC090599 Homo sapi
	888	18	1.1	165350	8	AC150788 AC150788 Oryza sat
	889	18	1.1	165378	9	AC129805 AC129805 Homo sapi
c	890	18	1.1	165488	10	AL807810 AL807810 Mouse DNA
	891	18	1.1	165527	2	AC109468 AC109468 Homo sapi
c	892	18	1.1	165575	2	AC007994 AC007994 Mus muscu
c	893	18	1.1	165701	8	AP004357 AP004357 Oryza sat
c	894	18	1.1	165854	9	AC073043 AC073043 Homo sapi
c	895	18	1.1	166054	9	AC069550 AC069550 Sequence
c	896	18	1.1	166077	5	BX470143 BX470143 Zebrafish
	897	18	1.1	166108	2	AC114304 AC114304 Homo sapi
	898	18	1.1	166219	9	AC003084 AC003084 Homo sapi
c	899	18	1.1	166323	2	AC142439 AC142439 Rattus no
	900	18	1.1	166659	9	AC104161 AC104161 Homo sapi
c	901	18	1.1	166763	2	AC112941 AC112941 Mus muscu
c	902	18	1.1	167140	5	BX248985 BX248985 Zebrafish
	903	18	1.1	167683	2	AC079251 AC079251 Homo sapi
	904	18	1.1	167834	2	AC148164 AC148164 Zea mays
c	905	18	1.1	168108	9	AC104119 AC104119 Homo sapi
c	906	18	1.1	168127	10	AC117243 AC117243 Mus muscu
c	907	18	1.1	168139	2	AC118638 AC118638 Mus muscu
	908	18	1.1	168177	2	AC023914 AC023914 Homo sapi
	909	18	1.1	168339	2	BX649454 BX649454 Danio rer
c	910	18	1.1	168360	4	AC145183 AC145183 Macropus
	911	18	1.1	168406	2	AC090770 AC090770 Homo sapi
	912	18	1.1	168476	9	AC011260 AC011260 Homo sapi
c	913	18	1.1	168535	8	AP006235 AP006235 Oryza sat
c	914	18	1.1	169082	10	AC130538 AC130538 Mus muscu
	915	18	1.1	169155	5	BX088685 BX088685 Zebrafish
c	916	18	1.1	169207	9	AC007490 AC007490 Homo sapi
	917	18	1.1	169365	2	AC023341 AC023341 Homo sapi
	918	18	1.1	169571	9	AC020687 AC020687 Homo sapi
	919	18	1.1	169746	2	AC108911 AC108911 Mus muscu
	920	18	1.1	169753	9	AC087506 AC087506 Homo sapi
c	921	18	1.1	170219	9	AC091991 AC091991 Homo sapi
c	922	18	1.1	170337	2	AP001378 AP001378 Homo sapi
c	923	18	1.1	170432	2	AC023322 AC023322 Homo sapi
c	924	18	1.1	170490	2	AC022042 AC022042 Homo sapi
c	925	18	1.1	170522	9	AL138708 AL138708 Human DNA
c	926	18	1.1	170741	10	AC130212 AC130212 Mus muscu
c	927	18	1.1	170745	2	AC120835 AC120835 Rattus no
c	928	18	1.1	170780	9	CNS01RH7 AL161663 Human chr
c	929	18	1.1	170781	9	AC013473 AC013473 Homo sapi
	930	18	1.1	170893	2	CR626910 CR626910 Danio rer
	931	18	1.1	171196	2	AP001369 AP001369 Homo sapi
	932	18	1.1	171430	2	AC110599 AC110599 Homo sapi
	933	18	1.1	171501	9	AL359704 AL359704 Human DNA
	934	18	1.1	171653	9	AC080162 AC080162 Homo sapi
	935	18	1.1	171850	2	AC021405 AC021405 Homo sapi
	936	18	1.1	171941	2	AC026531 AC026531 Homo sapi
c	937	18	1.1	172290	2	AC021728 AC021728 Homo sapi
c	938	18	1.1	172298	2	AC009556 AC009556 Homo sapi
c	939	18	1.1	172378	2	AC021696 AC021696 Homo sapi
c	940	18	1.1	172745	9	AC010591 AC010591 Homo sapi
	941	18	1.1	173180	2	AC147981 AC147981 Rattus no
c	942	18	1.1	173805	2	AL606966 AL606966 Homo sapi
	943	18	1.1	173816	2	AC141887 AC141887 Mus muscu
c	944	18	1.1	174176	5	AL772340 AL772340 Zebrafish
	945	18	1.1	174239	2	AC073830 AC073830 Homo sapi
	946	18	1.1	174304	9	AL450327 AL450327 Human DNA
	947	18	1.1	174504	2	AC015964 AC015964 Homo sapi
c	948	18	1.1	174711	9	AC026639 AC026639 Homo sapi
	949	18	1.1	174736	2	AC132924 AC132924 Homo sapi
	950	18	1.1	174799	2	AC142548 AC142548 Homo sapi
	951	18	1.1	175109	2	AC124279 AC124279 Homo sapi
c	952	18	1.1	175132	9	AL359641 AL359641 Human DNA
	953	18	1.1	175177	2	AC147852 AC147852 Oryctolag
	954	18	1.1	175368	9	CNS01DWF AL137164 Human chr
c	955	18	1.1	175378	2	AC113179 AC113179 Mus muscu
	956	18	1.1	175378	2	AC150490 AC150490 Bos tauru
	957	18	1.1	175495	5	BX001050 BX001050 Zebrafish
	958	18	1.1	175543	2	AC073378 AC073378 Homo sapi
c	959	18	1.1	175555	8	OSJN00237 AL731597 Oryza sat
c	960	18	1.1	175609	2	AC024663 AC024663 Homo sapi
	961	18	1.1	175631	9	AC023511 AC023511 Homo sapi
c	962	18	1.1	175832	9	AC023080 AC023080 Homo sapi
	963	18	1.1	175835	2	AC024074 AC024074 Homo sapi
	964	18	1.1	176249	2	AC069497 AC069497 Homo sapi
	965	18	1.1	176268	5	AL954175 AL954175 Zebrafish
	966	18	1.1	176466	9	AL161733 AL161733 Human DNA
	967	18	1.1	176555	9	AC096579 AC096579 Homo sapi
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969	18	1.1	176757	4	AC095025	AC095025 Sus scrof
970	18	1.1	176932	9	HS121G13	Z86062 Human DNA s
971	18	1.1	177003	9	AL590095	AL590095 Human DNA
c 972	18	1.1	177018	2	AC103584	AC103584 Bos tauru
973	18	1.1	177098	10	AL731695	AL731695 Mouse DNA
974	18	1.1	177171	2	AC128176	AC128176 Rattus no
975	18	1.1	177363	9	AC073856	AC073856 Homo sapi
c 976	18	1.1	177471	9	AC007446	AC007446 Homo sapi
c 977	18	1.1	177627	2	AC148261	AC148261 Callithri
978	18	1.1	177664	2	AC015749	AC015749 Homo sapi
979	18	1.1	177914	2	AC080141	AC080141 Mus muscu
c 980	18	1.1	178171	2	AC026961	AC026961 Homo sapi
981	18	1.1	178502	10	AC120397	AC120397 Mus muscu
982	18	1.1	178676	2	AC026965	AC026965 Homo sapi
c 983	18	1.1	178688	2	AL713893	AL713893 Homo sapi
984	18	1.1	178896	8	AP005709	AP005709 Oryza sat
c 985	18	1.1	179030	9	AC019254	AC019254 Homo sapi
986	18	1.1	179085	9	AC011611	AC011611 Homo sapi
987	18	1.1	179138	2	AC121439	AC121439 Rattus no
988	18	1.1	179344	2	AC147979	AC147979 Rattus no
c 989	18	1.1	179358	9	AP001496	AP001496 Homo sapi
c 990	18	1.1	179503	2	AC140790	AC140790 Gallus ga
c 991	18	1.1	179773	2	AC116041	AC116041 Papio ham
992	18	1.1	179964	9	AL606527	AL606527 Human DNA
c 993	18	1.1	180000	1	AF322012S1	AF322012 Bradyrhiz
c 994	18	1.1	180137	2	BX957257	BX957257 Danio rer
995	18	1.1	180192	2	AC058810	AC058810 Homo sapi
c 996	18	1.1	180233	9	AC011767	AC011767 Homo sapi
997	18	1.1	180398	2	AC140262	AC140262 Mus muscu
998	18	1.1	180526	2	AC136083	AC136083 Rattus no
c 999	18	1.1	180793	2	AC064812	AC064812 Homo sapi
1000	18	1.1	181058	2	AC068118	AC068118 Homo sapi

ALIGNMENTS

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RESULT 1
AX090311
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DEFINITION  Sequence 4 from Patent WO0116308.
ACCESSION   AX090311
VERSION     AX090311.1  GI:13444180
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Lassner,M. and van Eenennaam,A.
  TITLE     Plant sterol acyltransferases
  JOURNAL   Patent: WO 0116308-A 4 08-MAR-2001;
            MONSANTO COMPANY (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 1641;  DB 6;  Length 1641;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1641;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
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Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
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Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
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Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
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Qy        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300
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Db        241 AAGCTTCTTTCTGCTGTCAACTGCTGGTTTAAGTGTATGGTGCTAGATCCTTATAATCAA 300

Qy        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360
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Db        301 ACAGACCATCCCGAGTGTAAGTCACGGCCTGACAGTGGTCTTTCAGCCATCACAGAATTG 360

Qy        361 GATCCAGGTTACATAACAGGTCCTCTTTCTACTGTCTGGAAAGAGTGGCTTAAGTGGTGT 420
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Qy        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480
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Db        421 GTTGAGTTTGGTATAGAAGCAAATGCAATTGTCGCTGTTCCATACGATTGGAGATTGTCA 480

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Db        601 TTCAGATACTTTCTGGAATGGCTGAGGCTAGAAATTGCACCAAAACATTATTTGAAGTGG 660

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Qy        721 GCAATCAAATCTACTCTCTCTGGTGTAACGTTTGGCCTTCCTGTTTCTGAGGGAACTGCT 780
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Qy        841 AAGGGTGATAACACATCCTGGACGCATTTTTCTGGGGGTGCTGCAAAGAAAGATAAGCGC 900
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Qy        901 GTATACCACTGTGATGAAGAGGAATATCAATCAAAATATTCTGGCTGGCCGACAAATATT 960
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Db        961 ATTAACATTGAAATTCCTTCCACTAGCGTTACAGAAACAGCTCTAGTCAACATGACCAGC 1020

Qy       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080
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Db       1021 ATGGAATGTGGCCTTCCCACCCTTTTGTCTTTCACAGCCCGTGAACTAGCAGATGGGACT 1080

Qy       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140
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Db       1081 CTTTTCAAAGCAATAGAAGACTATGACCCAGATAGCAAGAGGATGTTACACCAGTTAAAG 1140

Qy       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200
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Db       1141 AAGTTGTATCATGATGACCCTGTTTTTAATCCTCTGACTCCTTGGGAGAGACCACCTATA 1200

Qy       1201 AAAAATGTATTTTGCATATATGGTGCTCATCTAAAGACAGAGGTTGGTTATTACTTTGCC 1260
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Qy       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320
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Db       1261 CCAAGTGGCAAACCTTATCCTGATAATTGGATCATCACGGATATCATTTACGAAACTGAA 1320

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Qy       1501 GTTGATCATGAGCATGGGTCAGACATCATAGCTAACATGACAAAAGCACCAAGGGTTAAG 1560
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Qy       1561 TACATAACCTTTTATGAAGACTCTGAGAGCATTCCGGGGAAGAGAACCGCAGTCTGGGAG 1620
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Qy       1621 CTTGATAAAAGTGGGTATTAA 1641
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RESULT 2
BD271623
LOCUS BD271623 3896 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271623
VERSION BD271623.1 GI:33081391
KEYWORDS JP 2002541783-A/8.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 3896)
AUTHORS Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
TITLE Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme
JOURNAL Patent: JP 2002541783-A 8 10-DEC-2002;
BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/8
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR 07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI ,HANS RONNE,STEN STYMNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
Novel class enzyme in biosynthesis pathway of triacrylglycerol
CC production
CC and recombinant DNA molecule encoding the enzyme FH Key Location/Qualifiers
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FT /organism='Arabidopsis thaliana (thale cress)'.
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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ORIGIN

Query Match 14.8%; Score 243; DB 6; Length 3896;
Best Local Similarity 100.0%; Pred. No. 1.2e-130;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60

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Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
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Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
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Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAG 243
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Db        241 AAG 243
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RESULT 3
BD271633
LOCUS BD271633 3896 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme.
ACCESSION BD271633
VERSION BD271633.1 GI:33081401
KEYWORDS JP 2002541783-A/18.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 3896)
AUTHORS Dahlqvist,A., Stahl,U., Lenman,M., Banas,A., Ronne,H. and Stymne,S.
TITLE Novel class enzyme in biosynthesis pathway of triacrylglycerol production and recombinant DNA molecule encoding the enzyme
JOURNAL Patent: JP 2002541783-A 18 10-DEC-2002;
BASF PLANT SCIENCE GMBH
COMMENT OS Arabidopsis thaliana (thale cress)
PN JP 2002541783-A/18
PD 10-DEC-2002
PF 28-MAR-2000 JP 2000609586
PR 01-APR-1999 EP 99106656.4,10-JUN-1999 EP 99111321.8 PR 07-FEB-2000 US 60/180687
PI ANDERS DAHLQVIST,ULF STAHL,MARIT LENMAN,ANTONI BANAS PI ,HANS RONNE,STEN STYMNE
PC C12N15/09,A01H5/00,C12N1/19,C12N5/10,C12N9/10,C12P7/64// PC (C12P7/64,C12R1:645),(C12P7/64,C12R1:91),C12N15/00,C12N5/00 CC
Novel class enzyme in biosynthesis pathway of triacrylglycerol
CC production
CC and recombinant DNA molecule encoding the enzyme FH Key Location/Qualifiers
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FT /organism='Arabidopsis thaliana (thale cress)'.
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
ORIGIN

Query Match 14.8%; Score 243; DB 6; Length 3896;

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  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
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Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
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Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAG 243
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Db        241 AAG 243


RESULT 4
AX037587
LOCUS       AX037587               3896 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 11 from Patent WO0060095.
ACCESSION   AX037587
VERSION     AX037587.1  GI:11227006
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Banas,A., Stahl,U., Stymne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
  TITLE     A new class of enzymes in the biosynthetic pathway for the
            production of triacylglycerol and recombinant dna molecules
            encoding these enzymes
  JOURNAL   Patent: WO 0060095-A 11 12-OCT-2000;
            BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
            STYMNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
            ANDERS (SE)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match            14.8%;  Score 243;  DB 6;  Length 3896;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-130;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
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Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
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Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAG 243
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Db        241 AAG 243


RESULT 5
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LOCUS       AX037606               3896 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 30 from Patent WO0060095.
ACCESSION   AX037606
VERSION     AX037606.1  GI:11227020
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Banas,A., Stahl,U., Stymne,S., Lenman,M., Ronne,H. and Dahlqvist,A.
  TITLE     A new class of enzymes in the biosynthetic pathway for the
            production of triacylglycerol and recombinant dna molecules
            encoding these enzymes
  JOURNAL   Patent: WO 0060095-A 30 12-OCT-2000;
            BASF PLANT SCIENCE GMBH (DE) ; BANAS ANTONI (PL) ; STAHL ULF (SE) ;
            STYMNE STEN (SE) ; LENMAN MARIT (SE) ; RONNE HANS (SE) ; DAHLQVIST
            ANDERS (SE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:3702"
ORIGIN

  Query Match            14.8%;  Score 243;  DB 6;  Length 3896;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-130;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
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Db         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240

Qy        241 AAG 243
              |||
Db        241 AAG 243


RESULT 6
AC003027
LOCUS       AC003027             119914 bp    DNA     linear   PLN 30-OCT-2002
DEFINITION  Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence,
            complete sequence.
ACCESSION   AC003027
VERSION     AC003027.1  GI:4079614
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
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            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,
            Au,M., Araujo,R., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
            Oji,O., Osborne,B.I., Shinn,P., Sun,H., Toriumi,M., Vyotskaia,V.,
            Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1997) Biochemistry, Stanford University/DNA
            Sequencing and Technology Center, 855 California Avenue, Palo Alto,
            CA 94304, USA
REFERENCE   3  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1998) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
REFERENCE   4  (bases 1 to 119914)
  AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,
            Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,
            Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.,
            Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JAN-1999) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
COMMENT     On Dec 30, 1998 this sequence version replaced gi:2734094.
            Bases 1-9262 of clone F21M11 overlap with bases 68998-78259 of
            'TAMU' BAC clone F20D22 (AC002411) and bases 119525-119914 of clone
            F21M11 overlap with bases 1-389 of 'TAMU' BAC clone F21B7
            (AC002560).
            e-mail for correspondence: arab@sequence.stanford.edu
            Genes with similarity to proteins in the databases are described as
            'putative', '-like' or 'similar to'.  Genes that have EST
            similarity but no significant protein similarity are described as
            'unknown proteins'.  Genes that are annotated based only on gene
            prediction software are described as 'hypothetical proteins'.
            The software programs used to predict genes include:  Grail
            (Informatics Group, Oak Ridge National Laboratory,
            http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
            http://gnomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev
            & A.Salamov, Sanger Centre,  http://genomic.sanger.ac.uk/), and
            NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
            Denmark,http://www.cbs.dtu.dk/NetPlantGene.html).
FEATURES              Location/Qualifiers
     source           1. .119914
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                      /mol_type="genomic DNA"
                      /cultivar="Columbia"
                      /db_xref="taxon:3702"
                      /chromosome="I"
                      /clone="F21M11"
     misc_feature     1. .9262
                      /note="overlap with bases 68998-78259 of 'IGF' BAC clone
                      F21M11."
     misc_feature     1. .7000
                      /note="Proteins in this region are annotated in the F21M11
                      entry, AC002411."
     gene             7684. .10913
                      /gene="F21M11.1"
     CDS              join(7684. .7866,7965. .8027,8122. .8160,8250. .8381,
                      8458. .8728,8875. .9893,10003. .10256,10344. .10410,
                      10501. .10551,10685. .10781,10885. .10913)
                      /gene="F21M11.1"
                      /note="Hypothetical protein"
                      /codon_start=1
                      /protein_id="AAD10665.1"
                      /db_xref="GI:4204284"
                      /translation="MAPNLRIKKACDAMKLLGISETKTRAFLRKLLKTYENNWDFIEE
                      DAYKVLLDAIFDEADAQSTEKNKKEEEKKKKEEEKKSRSVATSRGRRKAPEPLVQDEE
                      DDMDEDEFPLKRRLRSRRGRASSSSSSSSSYNNEDLKTQPEEEDEDDGVTELPPLKRY
                      VRRNGERGLAMTVYNNASPSSSSRLSMEPEEVPPMVLLPAHPMETKVSEASALVILND
                      EPNIDHKPVISDTGNCSAPMLEMGKSNIHVQEWDWETKDILNDTTAMDVSPSSAIGES
                      SEHKVAAASVELASSTSGEAKICLSFAPATGETTNLHLPSMEDLRRAMEEKCLKSYKI
                      VHPEFSVLGFMKDMCSCYIDLAKNSTSQLLETETVCDMSKAGDESGAVGISMPLVVVP
                      ECEISGDGWKAISNMKDITAGEENVEIPWVNEINEKVPSRFRYMPHSFVFQDAPVIFS
                      LSSFSDEQSCSTSCIEDCLASEMSCNCAIGVDNGFAYTLDGLLKEEFLEARISEARDQ
                      RKQVLRFCEECPLERAKKVEILEPCKGHLKRGAIKECWFKCGCTKRCGNRVVQRGMHN
                      KLQVFFTPNGKGWGLRTLEKLPKGAFICEYIGEILTIPELYQRSFEDKPTLPVILDAH
                      WGSEERLEGDKALCLDGMFYGNISRFLNHRCLDANLIEIPVQVETPDQHYYHLAFFTT
                      RDIEAMEELAWDYGIDFNDNDSLMKPFDCLCGSRFCRNKKRSTKTMQILNKA"
     gene             13033. .14514
                      /gene="F21M11.2"
     mRNA             join(13033. .13488,13717. .13926,14139. .14514)
                      /gene="F21M11.2"
     CDS              join(13061. .13488,13717. .13926,14139. .14316)
                      /gene="F21M11.2"
                      /note="Similar to acid phosphatase; Location of ESTs
                      110C2T7 , gb|T42036, and 110C2XP, gb|AI100245"
                      /codon_start=1
                      /protein_id="AAD10666.1"
                      /db_xref="GI:4204285"
                      /translation="MDRTMFLSLTIASLLVGVVSAGDWNILNQLRGLGSSSSQNGIVS
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                      LHFGSMCCSKSKCDGMDAWIFDIDDTLLSTIPYHKKNGFFGGEKLNSTKFEDWIQKKK
                      APAVPHMKKLYHDIRERGIKIFLISSRKEYLRSATVDNLIQAGYYGWSNLMLRGLEDQ
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     gene             complement(14004. .16362)
                      /gene="F21M11.3"
     mRNA             complement(join(14004. .14312,14565. .14641,14787. .15831,
                      15906. .16006,16327. .16362))
                      /gene="F21M11.3"
     CDS              complement(join(14567. .14641,14787. .15831,15906. .16006,
                      16327. .16362))
                      /gene="F21M11.3"
                      /note="Unknown protein; Location of ESTs 40C3TT,
                      gb|AA728590 and40C3T7, gb|T04573"
                      /codon_start=1
                      /protein_id="AAD10667.1"
                      /db_xref="GI:4204286"
                      /translation="MLDQISGNHTHEKLSVETAEPHHLNDRVHIVEEIPKASVIPITE
                      ICDEAEEKCSPSTISRKRVTFDSKVKTYEHVVSEESVELSEEKNEEVESEKRSLKSSK
                      TDDQIIEVASNSSGSYPENHRYKNCRESDDDIEEDEFDCSDSDLDEDEEYYSDVGFSE
                      DSLHNPTKEVYTQDIGDKTEEIDSKLRRSNETVRDGNHYDGQGVLNPVENLTQWKSAK
                      SKGRTKQKQSQKENSNFIADQEEKRDSSSFGTDPQIDDITLSVKPKCRIEPKKLRNQE
                      LAVDASLSTWLSTSESGSECNSASMYTLTPEKLKSTSCYSKPLRINHDDRPVLCALTL
                      EDIKQFSATSTPRKSPSKSPDETPIIGTVGGYWGNRSKAIDCGSASSFKGIPNTSSKY
                      REDKSVNWHSTPFEARLEKALNNIDK"
     gene             complement(16835. .20238)
                      /gene="F21M11.4"
     CDS              complement(join(16835. .17185,17274. .17392,17491. .17656,
                      17795. .17885,17982. .18079,18175. .18361,18504. .18604,
                      18705. .19049,19134. .19349,19439. .19791,19862. .19967,
                      20188. .20238))
                      /gene="F21M11.4"
                      /note="Hypothetical protein"
                      /codon_start=1
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                      /db_xref="GI:4204288"
                      /translation="MGSSSPEARARAQVPSMILIFLEIICTVHVYTNRRKLNRDVLSA
                      NLNIPKRVTRRDLRFMESVISIYKSLNAAVSVHLPQLQIPNDCNYKNDALNNSNSPKH
                      GESEDSEMTDKDVSKRSGGTDSSSRDGSPLPTSEESDPRPKHQDWTEKQLSDHLLLYE
                      FESEYDAANHTPESYTEQAAKNVRDITASEQPSNAARKRICGDSFIQESSPNPKTQDP
                      TLLRLMESLRSDDPTDYVKAQNHQMVYFSFWVIYSFVLCLRSNNLRCVVIFCVQQLPK
                      SHTEQDSKRKRDITASDAMENHLKVPKRENNLMQKSADIDCNGKCSANSDDQLSEKIS
                      KALEQTSSNITICGFCQSARVSEATGEMLHYSRGRPVDGDDIFRSNVIHVHSACIEWA
                      PQVYYEGDTVKNLKAELARGMKIKCTKCSLKGAALGCFVKSCRRSYHVPCAREISRCR
                      WDYEDFLLLCPAHSSVKFPNEKSGHRVSRAEPLPKINPAELCSLEQTPAFTKELVLCG
                      SALSKSDKKLMESLAVRFNATISRYWNPSVTHVIASTDEKGACTRTLKVLMGILNGKW
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                     IINAAWMKASLKASQPVDEEPFEIQIDTQGCQDGPKTARLRAETNKPKLFEGLKFYFF
                     GDFYKGYKEDLQNLVKVAGGTILNTEDELGAESSNNVNDQRSSSIVVYNIDPPHGCAL
                     GEEVTIIWQRANDAEALASQTGSRLVGHTWVLESIAGYKLHPVIG"
     gene            20752. .24647
                     /gene="F21M11.5"
     CDS             join(20752. .20994,21362. .21497,21596. .21740,21825. .21994,
                     22102. .22178,22542. .22758,22920. .23064,23343. .23442,
                     23599. .23693,24021. .24072,24227. .24298,24441. .24647)
                     /gene="F21M11.5"
                     /note="Hypothetical protein"
                     /codon_start=1
                     /protein_id="AAD10668.1"
                     /db_xref="GI:4204287"
                     /translation="MGANSKSVTASFTVIAVFFLICGGRTAVEDETEFHGDYSKLSGI
                     IIPGFASTQLRAWSILDCPYTPLDFNPLDLVWLDTTKLLSAVNCWFKCMVLDPYNQTD
                     HPECKSRPDSGLSAITELDPGYITGPLSTVWKEWLKWCVEFGIEANAIVAVPYDWRLS
                     PTKLEERDLYFHKLKLTFETALKLRGGPSIVFAHSMGNNVFRYFLEWLRLEIAPKHYL
                     KWLDQHIHAYFAVGAPLLGSVEAIKSTLSGVTFGLPVSEGTARLLSNSFASSLWLMPF
                     SKNCKGDNTFWTHFSGGAAKKDKRVYHCDEEEYQSKYSGWPTNIINIEIPSTSARELA
                     DGTLFKAIEDYDPDSKRMLHQLKKYVPFFVIRNIAHRSSLAGFLLYHDDPVFNPLTPW
                     ERPPIKNVFCIYGAHLKTEVGYYFAPSGKPYPDNWIITDIIYETEGSLVSRSGTVVDG
                     NAGPITGDETVPYHSLSWCKNWLGPKVNITMAPQILIGKIKQQPEHDGSDVHVELNVD
                     HEHGSDIIANMTKAPRVKYITFYEDSESIPGKRTAVWELDKSGY"
     gene            27777. .28734
                     /gene="F21M11.6"
     mRNA            27777. .28734
                     /gene="F21M11.6"
     CDS             28007. .28465
                     /gene="F21M11.6"
                     /note="Unknown protein; Location of ESTs 203I24T7,
                     gb|H76794 and 203I24XP, gb|AA605510"
                     /codon_start=1
                     /protein_id="AAD10670.1"
                     /db_xref="GI:4204289"
                     /translation="MNTKTMRLPPRRVLTADKRKERDAFISSVTDNPPEIAKFPSPPP
                     KLVPPPVNPISKKSSTAAAEPIGSNQLMLAGYLSHEYLTQGTLFGEQWNQARAQAESS
                     KIKPSHTVEPAEECEPKRKRYREVANLLRSDGAQLPGIVNPAQLARFLKL"
     gene            complement(29264. .32033)
                     /gene="F21M11.7"
     CDS             complement(join(29264. .31015,31312. .31414,31484. .31587,

  Query Match           14.8%;  Score 243;  DB 8;  Length 119914;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-130;
  Matches  243;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20752 ATGGGAGCGAATTCGAAATCAGTAACGGCTTCCTTCACCGTCATCGCCGTTTTTTTCTTG 20811

Qy         61 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20812 ATTTGCGGTGGCCGAACTGCGGTGGAGGATGAGACCGAGTTTCACGGCGACTACTCGAAG 20871

Qy        121 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20872 CTATCGGGTATAATCATTCCGGGATTTGCGTCGACGCAGCTACGAGCGTGGTCGATCCTT 20931

Qy        181 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20932 GACTGTCCATACACTCCGTTGGACTTCAATCCGCTCGACCTCGTATGGCTAGACACCACT 20991

Qy        241 AAG 243
              |||
Db      20992 AAG 20994


RESULT 7
AX090361
LOCUS       AX090361                44 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 54 from Patent WO0116308.
ACCESSION   AX090361
VERSION     AX090361.1  GI:13444222
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lassner,M. and van Eenennaam,A.
  TITLE     Plant sterol acyltransferases
  JOURNAL   Patent: WO 0116308-A 54 08-MAR-2001;
            MONSANTO COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .44
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer"
ORIGIN

  Query Match           1.6%;  Score 27;  DB 6;  Length 44;
  Best Local Similarity  100.0%;  Pred. No. 0.0027;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGGAGCGAATTCGAAATCAGTAACG 27
              |||||||||||||||||||||||||||
Db         18 ATGGGAGCGAATTCGAAATCAGTAACG 44


RESULT 8
AX090362/c
LOCUS       AX090362                40 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 55 from Patent WO0116308.
ACCESSION   AX090362
VERSION     AX090362.1  GI:13444223
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lassner,M. and van Eenennaam,A.
  TITLE     Plant sterol acyltransferases
  JOURNAL   Patent: WO 0116308-A 55 08-MAR-2001;
            MONSANTO COMPANY (US)
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide primer"
ORIGIN

  Query Match           1.6%;  Score 26;  DB 6;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 0.011;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1616 GGGAGCTTGATAAAAGTGGGTATTAA 1641
              ||||||||||||||||||||||||||
Db         40 GGGAGCTTGATAAAAGTGGGTATTAA 15


RESULT 9
AF493159
LOCUS       AF493159                2609 bp    mRNA    linear   PLN 02-DEC-2002
DEFINITION  Medicago truncatula putative phosphatidylcholine acyltransferase
            mRNA, complete cds.
ACCESSION   AF493159
VERSION     AF493159.1  GI:25992000
KEYWORDS    .
SOURCE      Medicago truncatula (barrel medic)
  ORGANISM  Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE   1  (bases 1 to 2609)
  AUTHORS   Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriel,A.
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  TITLE     Acyltransferases involved in lipid (sterol) biosynthesis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2609)
  AUTHORS   Benveniste,P., Bouvier-Nave,P., Schaller,H. and Noiriel,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAR-2002) Plant Molecular Biology Institute, CNRS, 28
            rue Goethe, Strasbourg 67083, France
FEATURES             Location/Qualifiers
     source          1. .2609
                     /organism="Medicago truncatula"
                     /mol_type="mRNA"
                     /db_xref="taxon:3880"
                     /clone_lib="Samuel Roberts Noble Foundation Medicago
                     truncatula insect herbivory library (Korth, K., et al.,
                     unpublished)"
                     /note="fabaceae; sequence derived from EST clones BE321377
                     and BI267156"
     CDS             82. .1980
                     /note="enzyme involved in the metabolism of phospholipids
                     and sterols"
                     /codon_start=1
                     /product="putative phosphatidylcholine acyltransferase"
                     /protein_id="AAN77002.1"
                     /db_xref="GI:25992001"
                     /translation="MANKPFLIFSILLAFLAVAGGDSGQGSELDYSKLSGIIIPGFAS
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                     PDSGLSGITELDPGYITGPLSSVWKEWIKWCIEFGIEANAIIAVPYDWRLSPSMLEER
                     DLYFHKLKLTFETAFKLRGGPSLVFGHSLGNNVFRYFLEWLKLEIAPKHYIQWLDQHI
                     HAYFAVAAPLLGATETIEATLSGFTFGLPVSEGTARLMFNSFASSLWMMPFSKYCRAS
                     NKYWKHFSGGKQVGTNTYHCDEEEFKSNFSGWPTKIINIEIPSTRGFEAYPSFSEIPE
                     ANLSGMECGLPTQLSFSAREIADGSFFKAIEDYDPDSKRLLYQLEKSYLGDPVLNPLT
                     PWDRPPIKNVFCIYGSNSKTKVGYYFAPSGKPYPDNWIITDVVYEYEGSLVTRSGNLV
                     EGNPGSISGDETVPYNSLSWCKNWLGPKVNITRAPQSEHDGSDVQIDLNVEHHYGDDI
                     VPNMTRFPRVKYITYYEDSESLPGKRTAVWELDKANHRNIVRSSVLMRELWLEMWRDI
                     HPDAKSEFVTKAKRGPLRDEDCYWDYGKARCAWPEYCEYRYVFGDVHLGQSCRLRYTS
                     ADLLLHYL"
ORIGIN

  Query Match             1.5%;  Score 25;  DB 8;  Length 2609;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        627 GCTAGAAATTGCACCAAAACATTAT 651
              |||||||||||||||||||||||||
Db        687 GCTAGAAATTGCACCAAAACATTAT 711


RESULT 10
TRBVSGAAB
LOCUS       TRBVSGAAB               2638 bp    DNA     linear   INV 26-APR-1993
DEFINITION  T.brucei variant surface glycoprotein (VSG) basic copy (BC) DNA, 5'
            non-coding region.
ACCESSION   M16036
VERSION     M16036.1  GI:162431
KEYWORDS    antigen; basic-copy gene; glycoprotein; variant surface antigen;
            variant surface glycoprotein.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 2638)
  AUTHORS   Lee,M.G. and Van der Ploeg,L.H.
  TITLE     Frequent independent duplicative transpositions activate a single
            VSG gene
  JOURNAL   Mol. Cell. Biol. 7 (1), 357-364 (1987)
  MEDLINE   87172726
   PUBMED   3031467
COMMENT     Original source text: T.brucei (variant 118) DNA, clone 1.
FEATURES             Location/Qualifiers
     source          1. .2638
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5691"
ORIGIN

  Query Match             1.3%;  Score 21;  DB 3;  Length 2638;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1259 CCCCAAGTGGCAAACCTTATC 1279
              |||||||||||||||||||||
Db        239 CCCCAAGTGGCAAACCTTATC 259


RESULT 11
AC073993/c
LOCUS       AC073993               38785 bp    DNA     linear   PRI 09-JAN-2002
DEFINITION  Homo sapiens BAC clone RP11-674L1 from 2, complete sequence.
ACCESSION   AC073993
VERSION     AC073993.4  GI:15431257
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 38785)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 38785)
  AUTHORS   Grewal,N. and Haakenson,W.
  TITLE     The sequence of Homo sapiens BAC clone RP11-674L1
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 38785)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUL-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 38785)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 38785)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Sep 5, 2001 this sequence version replaced gi:15187296.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0674L01
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
```

```
          Mapping information for this clone was provided by Dr. John D.
          McPherson, Department of Genetics, Washington University, St. Louis
          MO.  For additional information about the map position of this
          sequence, see http://genome.wustl.edu/gsc

          SOURCE INFORMATION:
          The RPCI-11 human BAC library was made from the blood of one male
          donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
          Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
          approach for construction of bacterial artificial chromosome
          libraries.  Genomics 51:1-8.  The clone may be obtained either from
          Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
          and coworkers at the Roswell Park Cancer Institute
          (http://bacpac.med.buffalo.edu)
          VECTOR:  pBACe3.6
          NEIGHBORING SEQUENCE INFORMATION:
          The clone sequenced to the left is RP11-318K6, 2000 bp overlap; the
          clone sequenced to the right is RP11-70L16, 2000 bp overlap.
          Actual start of this clone is at base position 127793 of
          RP11-318K6; actual end is at base position 73456 of RP11-70L16.
FEATURES             Location/Qualifiers
     source          1. .38785
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /map="2"
                     /clone="RP11-674L1"
                     /clone_lib="RPCI-11"
     repeat_region   268. .567
                     /rpt_family="Alu"
     repeat_region   2001. .2022
                     /rpt_family="AT_rich"
     repeat_region   2012. .2491
                     /rpt_family="L1"
     repeat_region   2492. .3130
                     /rpt_family="L1"
     repeat_region   3134. .4785
                     /rpt_family="L1"
     repeat_region   4018. .4040
                     /rpt_family="(A)n"
     repeat_region   4434. .4467
                     /rpt_family="(TTTA)n"
     repeat_region   4834. .5194
                     /rpt_family="L1"
     repeat_region   5203. .5726
                     /rpt_family="L1"
     repeat_region   5858. .5911
                     /rpt_family="L1"
     repeat_region   5912. .6199
                     /rpt_family="Alu"
     repeat_region   6193. .6234
                     /rpt_family="AT_rich"
     repeat_region   6200. .7682
                     /rpt_family="L1"
     repeat_region   7694. .7752
                     /rpt_family="Alu"
     repeat_region   7753. .8630
                     /rpt_family="ERVK"
     repeat_region   8631. .8888
                     /rpt_family="Alu"
     repeat_region   8891. .9599
                     /rpt_family="L1"
     repeat_region   9600. .9800
                     /rpt_family="L1"
     repeat_region   9801. .9917
                     /rpt_family="L1"
     misc_feature    9803. .9891
                     /note="match to EST AA435786 (NID:g2140700) zt77e09.s1"
     repeat_region   9926. .9993
                     /rpt_family="L1"
     repeat_region   10539. .10613
                     /rpt_family="Mariner"
     repeat_region   10790. .11651
                     /rpt_family="L1"
     repeat_region   10796. .10819
                     /rpt_family="AT_rich"
     repeat_region   11605. .11633
                     /rpt_family="AT_rich"
     repeat_region   11710. .12008
                     /rpt_family="Alu"
     repeat_region   11872. .11898
                     /rpt_family="AT_rich"
     repeat_region   12089. .12128
                     /rpt_family="AT_rich"
     repeat_region   12239. .12292
                     /rpt_family="AT_rich"
     repeat_region   12390. .12435
                     /rpt_family="AT_rich"
     repeat_region   13069. .13380
                     /rpt_family="Alu"
     repeat_region   13074. .13096
                     /rpt_family="(TTTA)n"
     repeat_region   13951. .14051
                     /rpt_family="MIR"
     repeat_region   14347. .14913
                     /rpt_family="L1"
     repeat_region   14605. .14642
                     /rpt_family="AT_rich"
     repeat_region   14987. .15230
                     /rpt_family="L2"
     repeat_region   15310. .15436
                     /rpt_family="MIR"
     repeat_region   15814. .16114
                     /rpt_family="Alu"
     repeat_region   15929. .15952
                     /rpt_family="AT_rich"
     misc_feature    15957. .16257
                     /note="match to EST AA435786 (NID:g2140700) zt77e09.s1"
     repeat_region   17336. .17461
                     /rpt_family="L2"
     repeat_region   17706. .17835
                     /rpt_family="MER2_type"
     misc_feature    17778. .18022
                     /note="match to EST Z21373 (NID:g28116)"
     repeat_region   17838. .17915
                     /rpt_family="(TATG)n"
     repeat_region   18345. .18390
                     /rpt_family="ERVL"
     repeat_region   19325. .19452
                     /rpt_family="L1"
     repeat_region   20075. .20610
                     /rpt_family="L1"
     repeat_region   20838. .21123
                     /rpt_family="Alu"
     repeat_region   21120. .21141
                     /rpt_family="AT_rich"
     repeat_region   22354. .22466
                     /rpt_family="ERVL"
     repeat_region   22996. .23045
                     /rpt_family="AT_rich"
     repeat_region   23021. .23573
                     /rpt_family="L1"
     repeat_region   23574. .24284
                     /rpt_family="ERV1"
     repeat_region   24285. .24520
                     /rpt_family="L1"
     repeat_region   25264. .25285
                     /rpt_family="(A)n"
     repeat_region   25737. .25787

  Query Match             1.3%;  Score 21;  DB 9;  Length 38785;
  Best Local Similarity   100.0%;  Pred. No. 8.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        509 ACTTTCACAAGCTCAAGTTGA 529
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                    ||||||||||||||||||||
Db      28342 ACTTTCACAAGCTCAAGTTGA 28322


RESULT 12
AL929207/c
LOCUS       AL929207               70206 bp    DNA     linear   VRT 29-JUL-2003
DEFINITION  Zebrafish DNA sequence from clone CH211-214P16 in linkage group 17
            Contains a novel gene for a protein similar to human mitochondrial
            isoleucine tRNA synthetase, a novel gene similar to RAB3GAP (RAB3
            GTPase-activating protein), a novel gene similar to PPP1CB (protein
            phosphatase 1, catalytic subunit, beta isoform), two novel genes
            and a CpG island, complete sequence.
ACCESSION   AL929207
VERSION     AL929207.5  GI:25252137
KEYWORDS    HTG; CpG island; GTPase-activating; isoleucine tRNA synthetase;
            PPP1CB; protein phosphatase; RAB3; RAB3GAP.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 70206)
  AUTHORS   Babbage,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 24, 2002 this sequence version replaced gi:25168772.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest, except on the rare
            occasion of the clone being a YAC.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep CH211-214P16 is
            from a CHORI-211 BAC library
            VECTOR: pTARBAC2.1
            IMPORTANT: This sequence is not the entire insert of clone
            CH211-214P16 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true left end of clone CH211-214P16 is at 1 in this sequence.
            The true left end of clone DKEY-98G12 is at 68207 in this sequence.
            Clone-derived Zebrafish pUC subclones occasionally display
            inconsistency over the length of mononucleotide A/T runs and
            conserved TA repeats. Where this is found the longest good quality
            representation will be submitted.
            Repeat names beginning 'Dr' were identified by the Recon repeat
            discovery system (Zhirong Bao and Sean Eddy, submitted), and those
            beginning 'drr' were identified by Rick Waterman (Stephen Johnson
            lab, WashU).  For further information see
            http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
            -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            --------------.
FEATURES             Location/Qualifiers
     source          1. .70206
                     /organism="Danio rerio"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7955"
                     /clone="CH211-214P16"
                     /clone_lib="CHORI-211"
     repeat_region   432. .834
                     /note="Dr000004 repeat: matches 1. .442 of consensus"
     repeat_region   850. .1045
                     /note="Dr000012 repeat: matches 211. .415 of consensus"
     repeat_region   complement(1148. .1352)
                     /note="TDR16 repeat: matches 41. .254 of consensus"
     repeat_region   1526. .1537
                     /note="2.0 copies 6 mer GCGTTT 24% conserved"
     repeat_region   1542. .1561
                     /note="5.0 copies 4 mer AGAC 22% conserved"
     repeat_region   1544. .1566
                     /note="2.6 copies 9 mer ACAGAAAGA 30% conserved"
     repeat_region   2246. .2256
                     /note="3.7 copies 3 mer TTA 22% conserved"
     repeat_region   2291. .2318
                     /note="2.3 copies 12 mer ATTTGTATATTA 47% conserved"
     repeat_region   2300. .2318
                     /note="3.2 copies 6 mer TTAATT 22% conserved"
     repeat_region   2320. .2519
                     /note="Dr000276 repeat: matches 1. .198 of consensus"
     repeat_region   2520. .2687
                     /note="TDR7 repeat: matches 2. .463 of consensus"
     repeat_region   complement(2689. .2787)
                     /note="ACROBAT1 repeat: matches 779. .877 of consensus"
     repeat_region   2714. .2800
                     /note="ACROBAT1 repeat: matches 779. .865 of consensus"
     repeat_region   2871. .2903
                     /note="3.0 copies 11 mer ATTTATTTTT 39% conserved"
     repeat_region   2879. .2893
                     /note="3.8 copies 4 mer TTTA 23% conserved"
     repeat_region   3017. .3026
                     /note="2.0 copies 5 mer TAATT 20% conserved"
     repeat_region   3414. .3427
                     /note="2.0 copies 7 mer GTTTTGG 28% conserved"
     repeat_region   3805. .3908
                     /note="Dr000349 repeat: matches 5. .108 of consensus"
     repeat_region   3909. .3924
                     /note="16.0 copies 1 mer T 32% conserved"
     repeat_region   4149. .4163
                     /note="5.0 copies 3 mer TAT 23% conserved"
     repeat_region   4285. .4301
                     /note="2.8 copies 6 mer TTTATG 27% conserved"
     gene            complement(4889. .6150)
                     /gene="SI:zC214P16.1"
     mRNA            complement(join(4889. .5336,6065. .6150))
                     /gene="SI:zC214P16.1"
                     /product="SI:zC214P16.1 (novel protein)"
                     /note="match: ESTs: Em:BI842764 Em:AL927523 Em:BM081467
                     Em:BI472229"
                     /evidence=not_experimental
     repeat_region   5000. .5012
                     /note="13.0 copies 1 mer T 26% conserved"
     CDS             complement(join(5175. .5336,6065. .6136))
                     /gene="SI:zC214P16.1"
                     /codon_start=1
                     /evidence=not_experimental
                     /product="SI:zC214P16.1 (novel protein)"
                     /protein_id="CAD61266.1"
                     /db_xref="GI:27884147"
                     /translation="MKMNQILTLCLGMLLLTLPFSTSEDKGSAKDGEQKPASQPTNNT
                     NTNTAGATDAAGLDVLPTMLCLLIPAATLSFMH"
     repeat_region   5462. .5475
                     /note="2.8 copies 5 mer TTTTG 28% conserved"
     repeat_region   5514. .5546
                     /note="3.3 copies 10 mer TTAAAGTTAT 48% conserved"
     repeat_region   5618. .5891
                     /note="ANGEL repeat: matches 13. .312 of consensus"
     repeat_region   6017. .6028
                     /note="12.0 copies 1 mer A 24% conserved"
```

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     repeat_region   complement(6575. .6665)
                     /note="ANGEL repeat: matches 213. .315 of consensus"
     repeat_region   complement(6663. .6730)
                     /note="Dr000403 repeat: matches 3. .71 of consensus"
     repeat_region   6724. .6907
                     /note="ANGEL repeat: matches 93. .290 of consensus"
     repeat_region   7200. .7215
                     /note="3.2 copies 5 mer GCTGT 32% conserved"
     repeat_region   7237. .7246
                     /note="2.5 copies 4 mer TCTG 20% conserved"
     gene            complement(7273. .7742)
                     /gene="SI:zC214P16.2"
     mRNA            complement(join(7273. .7442,7637. .7742))
                     /gene="SI:zC214P16.2"
                     /product="SI:zC214P16.2 (novel protein)"
                     /note="match: ESTs: Em:AL925814"
                     /evidence=not_experimental
     CDS             complement(join(7299. .7442,7637. .7699))
                     /gene="SI:zC214P16.2"
                     /codon_start=1
                     /evidence=not_experimental
                     /product="SI:zC214P16.2 (novel protein)"
                     /protein_id="CAD61267.1"
                     /db_xref="GI:27884148"
                     /translation="MNKLWILCFVVLIMSKPFSTEESQKSSENTVPSPSASTNSSAVG
                     LSPVPKTLYLLFPAATLGFIHSRS"
     repeat_region   7482. .7492
                     /note="2.2 copies 5 mer ATAAA 22% conserved"
     repeat_region   7537. .7554
                     /note="2.0 copies 9 mer TAAAATATG 36% conserved"
     repeat_region   7709. .7719
                     /note="2.2 copies 5 mer TGTGT 22% conserved"
     repeat_region   8395. .8405
                     /note="11.0 copies 1 mer T 22% conserved"
     repeat_region   complement(8440. .9186)
                     /note="Dr000011 repeat: matches 247. .1027 of consensus"
     repeat_region   complement(9184. .9319)
                     /note="Dr000068 repeat: matches 1. .139 of consensus"
     repeat_region   9499. .9512
                     /note="4.7 copies 3 mer GGA 28% conserved"
     gene            9569. .25705
                     /gene="SI:zC214P16.3"
     mRNA            join(<9569. .9748,10757. .10879,11056. .11209,12314. .12462,
                     12879. .12928,13026. .13135,13238. .13325,13691. .13806,
                     13879. .14048,14732. .14822,14916. .15067,16099. .16259,
                     16353. .16455,19448. .19541,19673. .19781,19865. .19967,
                     20256. .20381,21436. .21567,21984. .22090,22165. .22310,
                     22388. .22578,24849. .24993,25433. .25705)
                     /gene="SI:zC214P16.3"
                     /product="SI:zC214P16.3 (novel protein similar to human
                     mitochondrial isoleucine tRNA synthetase)"
                     /note="match: cDNAs: Em:AK001188 Em:BC027432
                     match: ESTs: Em:BJ003540 Em:BJ000714 Em:AI522531
                     Em:AL920795 Em:AL924967 Em:BJ008909 Em:CA357288
                     Em:BI888106 Em:AL919151"
                     /evidence=not_experimental
     CDS             join(<9569. .9748,10757. .10879,11056. .11209,12314. .12462,
                     12879. .12928,13026. .13135,13238. .13325,13691. .13806,
                     13879. .14048,14732. .14822,14916. .15067,16099. .16259,
                     16353. .16455,19448. .19541,19673. .19781,19865. .19967,

  Query Match             1.3%;  Score 21;  DB 5;  Length 70206;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        302 CAGACCATCCCGAGTGTAAGT 322
              |||||||||||||||||||||
Db      41763 CAGACCATCCCGAGTGTAAGT 41743


RESULT 13
AL603869
LOCUS       AL603869               74349 bp    DNA     linear   PRI 27-SEP-2001
DEFINITION  Human DNA sequence from clone RP11-202P3 on chromosome 13, complete
            sequence.
ACCESSION   AL603869
VERSION     AL603869.5  GI:15808267
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 74349)
  AUTHORS   Bates,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Sep 28, 2001 this sequence version replaced gi:15617331.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 13, constructed by the Sanger Centre Chromosome 13
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr13
            RP11-202P3 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            IMPORTANT: This sequence is not the entire insert of clone
            RP11-202P3 It may be shorter because we sequence overlapping
            sections only once, except for a short overlap.
            The true right end of clone RP11-202P3 is at 74349 in this
            sequence. The true right end of clone RP11-272M24 is at 2000 in
            this sequence.
FEATURES             Location/Qualifiers
     source          1. .74349
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /clone="RP11-202P3"
                     /clone_lib="RPCI-11.1"
ORIGIN

  Query Match             1.3%;  Score 21;  DB 9;  Length 74349;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1196 CTATAAAAAATGTATTTTGCA 1216
              |||||||||||||||||||||
Db      20995 CTATAAAAAATGTATTTTGCA 21015


RESULT 14
AP006356/c
LOCUS       AP006356               93398 bp    DNA     linear   PLN 22-JUL-2003
DEFINITION  Lotus corniculatus var. japonicus genomic DNA, chromosome 6,
            clone:LjT06I08, TM0082b, complete sequence.
ACCESSION   AP006356
```

```
VERSION     AP006356.1  GI:31580987
KEYWORDS    HTG.
SOURCE      Lotus corniculatus var. japonicus (Lotus japonicus)
  ORGANISM  Lotus corniculatus var. japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
            Lotus.
REFERENCE   1
  AUTHORS   Asamizu,E., Kato,T., Sato,S., Nakamura,Y., Kaneko,T. and Tabata,S.
  TITLE     Structural Analysis of a Lotus japonicus Genome. IV. Sequence
            Features and Mapping of seventy-three TAC clones which cover the
            7.5 Mb Regions of the Genome
  JOURNAL   DNA Res. (2003) In press
REFERENCE   2  (bases 1 to 93398)
  AUTHORS   Sato,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2003) Shusei Sato, Kazusa DNA Research Institute,
            Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
            Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
            Fax:81-438-52-3934)
FEATURES             Location/Qualifiers
     source          1. .93398
                     /organism="Lotus corniculatus var. japonicus"
                     /mol_type="genomic DNA"
                     /variety="japonicus"
                     /db_xref="taxon:34305"
                     /chromosome="6"
                     /clone="LjT06I08"
                     /clone_lib="LjT library"
                     /note="TM0082b, a part of TAC clone:TM0082.~synonym: Lotus
                     japonicus"
ORIGIN

  Query Match             1.3%;  Score 21;  DB 8;  Length 93398;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1102 TATGACCCAGATAGCAAGAGG 1122
              |||||||||||||||||||||
Db      29743 TATGACCCAGATAGCAAGAGG 29723


RESULT 15
AC006988
LOCUS       AC006988               107430 bp    DNA     linear   PRI 08-OCT-2003
DEFINITION  Homo sapiens BAC clone RP11-174I14 from 7, complete sequence.
ACCESSION   AC006988
VERSION     AC006988.3  GI:9857575
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 107430)
  AUTHORS   Sulston,J.E. and Wilson,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 107430)
  AUTHORS   Courtney,L., Merry,B. and Stoneking,T.
  TITLE     The sequence of Homo sapiens BAC clone RP11-174I14
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 107430)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-MAR-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 107430)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-AUG-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 107430)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-SEP-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 107430)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-APR-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   7  (bases 1 to 107430)
  AUTHORS   Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Aug 19, 2000 this sequence version replaced gi:6094669.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0174I14
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            The sequence of this clone was established as part of a mapping and
            sequencing collaboration between the NHGRI Chromosome 7 Mapping
            Project (Eric D. Green, Director), John D. McPherson in the
            Department of Genetics (Washington University), and the Washington
            University Genome Sequencing Center. For additional information
            about the map position of this sequence, see
            http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
            mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is CTA-326K9, 200 bp overlap the
            clone sequenced to the right is CTA-305H12, 200 bp overlap.  Actual
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO_NUC
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Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	18	1.1	153	4	US-09-513-999C-23083	Sequence 23083, A
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	7	18	1.1	241	4	US-09-389-681-371	Sequence 371, App
	8	18	1.1	241	4	US-09-620-405B-371	Sequence 371, App
	9	18	1.1	241	4	US-09-433-826B-371	Sequence 371, App
	10	18	1.1	241	4	US-09-604-287A-371	Sequence 371, App
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	12	18	1.1	241	4	US-09-590-751A-371	Sequence 371, App
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	16	18	1.1	451	4	US-09-606-421B-325	Sequence 325, App
	17	18	1.1	451	4	US-09-630-940B-325	Sequence 325, App
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	64	16	1.0	23	1	US-08-379-078-124	Sequence 124, App
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c	93	16	1.0	252	3	US-09-012-692-104	Sequence 104, App
c	94	16	1.0	252	3	US-08-906-613-104	Sequence 104, App
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157	16	1.0	531	4	US-09-216-003A-5	Sequence 5, Appli
158	16	1.0	531	4	US-09-667-857-5	Sequence 5, Appli
159	16	1.0	555	4	US-09-270-767-8811	Sequence 8811, Ap
160	16	1.0	555	4	US-09-270-767-24093	Sequence 24093, A
c 161	16	1.0	571	4	US-09-621-976-17179	Sequence 17179, A
c 162	16	1.0	591	4	US-09-710-279-3069	Sequence 3069, Ap
163	16	1.0	603	4	US-09-248-796A-2041	Sequence 2041, Ap
c 164	16	1.0	643	2	US-08-975-316-59	Sequence 59, Appl
c 165	16	1.0	643	4	US-09-615-192A-59	Sequence 59, Appl
c 166	16	1.0	643	4	US-09-169-789-59	Sequence 59, Appl
c 167	16	1.0	651	4	US-09-248-796A-3406	Sequence 3406, Ap
c 168	16	1.0	681	4	US-09-248-796A-2079	Sequence 2079, Ap
c 169	16	1.0	687	4	US-09-710-279-2935	Sequence 2935, Ap
c 170	16	1.0	687	4	US-09-710-279-3195	Sequence 3195, Ap
c 171	16	1.0	699	3	US-09-276-531-91	Sequence 91, Appl
c 172	16	1.0	702	3	US-09-134-001C-806	Sequence 806, App
173	16	1.0	711	3	US-08-823-120-5	Sequence 5, Appli
174	16	1.0	720	4	US-09-270-767-25226	Sequence 25226, A
c 175	16	1.0	724	3	US-08-858-207A-206	Sequence 206, App
c 176	16	1.0	756	4	US-09-543-681A-2342	Sequence 2342, Ap
177	16	1.0	768	4	US-09-248-796A-5524	Sequence 5524, Ap
c 178	16	1.0	784	4	US-10-101-464A-340	Sequence 340, App
179	16	1.0	795	4	US-09-266-965-57	Sequence 57, Appl
c 180	16	1.0	811	3	US-09-662-250A-15	Sequence 15, Appl
c 181	16	1.0	815	3	US-08-906-769-128	Sequence 128, App
c 182	16	1.0	815	3	US-08-906-616-128	Sequence 128, App
c 183	16	1.0	815	3	US-08-639-075A-128	Sequence 128, App
c 184	16	1.0	815	3	US-09-012-431-128	Sequence 128, App
c 185	16	1.0	815	3	US-09-012-692-128	Sequence 128, App
c 186	16	1.0	815	3	US-08-906-613-128	Sequence 128, App
c 187	16	1.0	871	4	US-09-270-767-2493	Sequence 2493, Ap
c 188	16	1.0	871	4	US-09-270-767-17775	Sequence 17775, A
c 189	16	1.0	903	3	US-09-134-001C-1925	Sequence 1925, Ap
c 190	16	1.0	915	4	US-09-462-845-8	Sequence 8, Appli
191	16	1.0	925	3	US-08-714-918-59	Sequence 59, Appl
192	16	1.0	925	3	US-09-265-315-59	Sequence 59, Appl
193	16	1.0	925	3	US-09-265-315-59	Sequence 59, Appl
194	16	1.0	925	3	US-09-266-417-59	Sequence 59, Appl
195	16	1.0	925	4	US-09-528-709-59	Sequence 59, Appl
196	16	1.0	925	4	US-09-527-745-59	Sequence 59, Appl
c 197	16	1.0	930	4	US-09-252-991A-11343	Sequence 11343, A
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c 199	16	1.0	945	2	US-08-967-101-160	Sequence 160, App
c 200	16	1.0	945	2	US-08-592-541-6	Sequence 6, Appli
c 201	16	1.0	945	2	US-08-592-541-160	Sequence 160, App
c 202	16	1.0	945	3	US-08-888-077A-10	Sequence 10, Appl
c 203	16	1.0	945	3	US-09-124-698-6	Sequence 6, Appli
c 204	16	1.0	945	3	US-09-124-698-160	Sequence 160, App
c 205	16	1.0	945	3	US-09-127-480-6	Sequence 6, Appli
c 206	16	1.0	945	3	US-09-127-480-160	Sequence 160, App
c 207	16	1.0	945	3	US-08-496-841C-6	Sequence 6, Appli
c 208	16	1.0	945	3	US-08-496-841C-160	Sequence 160, App
c 209	16	1.0	945	3	US-09-124-523-6	Sequence 6, Appli
c 210	16	1.0	945	3	US-09-124-523-160	Sequence 160, App
c 211	16	1.0	945	4	US-09-636-796A-6	Sequence 6, Appli
c 212	16	1.0	945	4	US-09-636-796A-160	Sequence 160, App
c 213	16	1.0	945	4	US-08-431-048F-6	Sequence 6, Appli
214	16	1.0	984	4	US-09-489-039A-1913	Sequence 1913, Ap
c 215	16	1.0	1029	4	US-09-107-532A-1842	Sequence 1842, Ap
216	16	1.0	1038	3	US-09-004-838-128	Sequence 128, App
217	16	1.0	1055	4	US-09-632-277A-1	Sequence 1, Appli
218	16	1.0	1071	4	US-09-270-767-1061	Sequence 1061, Ap
219	16	1.0	1071	4	US-09-270-767-16343	Sequence 16343, A
c 220	16	1.0	1084	3	US-08-604-789B-14	Sequence 14, Appl
c 221	16	1.0	1084	3	US-09-312-721A-14	Sequence 14, Appl
c 222	16	1.0	1084	4	US-09-733-300-14	Sequence 14, Appl
c 223	16	1.0	1086	3	US-09-134-001C-1208	Sequence 1208, Ap
224	16	1.0	1114	4	US-09-896-096A-2	Sequence 2, Appli
c 225	16	1.0	1122	4	US-09-248-796A-729	Sequence 729, App
c 226	16	1.0	1137	4	US-09-543-681A-432	Sequence 432, App
227	16	1.0	1164	2	US-08-794-796-1	Sequence 1, Appli
228	16	1.0	1182	4	US-09-248-796A-4758	Sequence 4758, Ap
c 229	16	1.0	1232	4	US-09-799-451-665	Sequence 665, App
230	16	1.0	1251	4	US-09-543-681A-848	Sequence 848, App
c 231	16	1.0	1275	4	US-09-248-796A-10014	Sequence 10014, A
c 232	16	1.0	1302	4	US-09-252-991A-15634	Sequence 15634, A
233	16	1.0	1347	3	US-09-286-529-18	Sequence 18, Appl
c 234	16	1.0	1359	4	US-09-328-352-3036	Sequence 3036, Ap
c 235	16	1.0	1377	4	US-09-252-991A-8614	Sequence 8614, Ap
236	16	1.0	1398	4	US-09-489-039A-264	Sequence 264, App
237	16	1.0	1462	4	US-09-270-767-9923	Sequence 9923, Ap
c 238	16	1.0	1476	4	US-09-248-796A-1686	Sequence 1686, Ap
c 239	16	1.0	1506	3	US-09-198-955A-13	Sequence 13, Appl
c 240	16	1.0	1506	3	US-09-694-531-13	Sequence 13, Appl
c 241	16	1.0	1506	4	US-10-072-152-13	Sequence 13, Appl
242	16	1.0	1524	4	US-09-248-796A-4180	Sequence 4180, Ap
c 243	16	1.0	1569	4	US-09-149-476-150	Sequence 150, App
244	16	1.0	1629	4	US-09-248-796A-2029	Sequence 2029, Ap
245	16	1.0	1659	4	US-09-252-991A-15717	Sequence 15717, A
246	16	1.0	1722	4	US-09-328-352-2294	Sequence 2294, Ap

c 247	16	1.0	1760	4	US-09-270-767-1590	Sequence 1590, Ap
c 248	16	1.0	1760	4	US-09-270-767-16872	Sequence 16872, A
249	16	1.0	1840	4	US-09-620-312D-320	Sequence 320, App
250	16	1.0	1859	3	US-09-286-529-19	Sequence 19, Appl
251	16	1.0	1921	2	US-08-557-128-11	Sequence 11, Appl
c 252	16	1.0	1964	4	US-09-799-451-39	Sequence 39, Appl
253	16	1.0	1971	4	US-10-140-002-139	Sequence 139, App
254	16	1.0	2017	4	US-09-404-879A-72	Sequence 72, Appl
255	16	1.0	2017	4	US-09-338-933-72	Sequence 72, Appl
256	16	1.0	2017	4	US-09-215-681-72	Sequence 72, Appl
257	16	1.0	2017	4	US-09-216-003A-72	Sequence 72, Appl
258	16	1.0	2017	4	US-09-667-857-72	Sequence 72, Appl
c 259	16	1.0	2022	4	US-09-583-110-199	Sequence 199, App
260	16	1.0	2118	4	US-09-800-729-34	Sequence 34, Appl
261	16	1.0	2124	4	US-09-248-796A-3684	Sequence 3684, Ap
c 262	16	1.0	2133	4	US-09-661-322A-41	Sequence 41, Appl
c 263	16	1.0	2180	2	US-09-003-217-1	Sequence 1, Appli
c 264	16	1.0	2180	3	US-09-218-942-1	Sequence 1, Appli
265	16	1.0	2189	4	US-09-106-568E-7	Sequence 7, Appli
266	16	1.0	2271	4	US-09-248-796A-3650	Sequence 3650, Ap
267	16	1.0	2375	4	US-08-956-171E-147	Sequence 147, App
268	16	1.0	2375	4	US-08-781-986A-147	Sequence 147, App
c 269	16	1.0	2538	4	US-09-248-796A-3859	Sequence 3859, Ap
c 270	16	1.0	2543	3	US-09-307-143-5	Sequence 5, Appli
271	16	1.0	2600	4	US-09-589-892B-1	Sequence 1, Appli
272	16	1.0	2873	3	US-08-630-915A-193	Sequence 193, App
273	16	1.0	2873	4	US-09-879-957-193	Sequence 193, App
c 274	16	1.0	2905	3	US-09-468-578-3	Sequence 3, Appli
c 275	16	1.0	2905	4	US-09-868-839-3	Sequence 3, Appli
c 276	16	1.0	2965	2	US-08-460-570-1	Sequence 1, Appli
c 277	16	1.0	2965	2	US-08-460-570-2	Sequence 2, Appli
c 278	16	1.0	2965	3	US-08-286-870A-1	Sequence 1, Appli
c 279	16	1.0	2965	3	US-08-286-870A-2	Sequence 2, Appli
c 280	16	1.0	3147	2	US-07-952-853-23	Sequence 23, Appl
c 281	16	1.0	3147	2	US-08-914-848-23	Sequence 23, Appl
c 282	16	1.0	3226	3	US-08-539-205A-5	Sequence 5, Appli
c 283	16	1.0	3226	4	US-09-392-163A-5	Sequence 5, Appli
284	16	1.0	3233	4	US-09-710-279-3586	Sequence 3586, Ap
c 285	16	1.0	3273	4	US-09-799-451-907	Sequence 907, App
c 286	16	1.0	3288	1	US-08-208-008C-3	Sequence 3, Appli
c 287	16	1.0	3632	4	US-09-710-279-4278	Sequence 4278, Ap
288	16	1.0	3633	4	US-09-710-279-4035	Sequence 4035, Ap
c 289	16	1.0	3722	4	US-10-164-595-9	Sequence 9, Appli
290	16	1.0	3767	4	US-09-710-279-4213	Sequence 4213, Ap
291	16	1.0	3781	4	US-09-710-279-3993	Sequence 3993, Ap
c 292	16	1.0	3805	4	US-09-710-279-3687	Sequence 3687, Ap
c 293	16	1.0	3862	4	US-10-164-595-5	Sequence 5, Appli
c 294	16	1.0	3877	2	US-08-599-895-1	Sequence 1, Appli
c 295	16	1.0	3877	3	US-09-211-290-1	Sequence 1, Appli
c 296	16	1.0	3877	3	US-09-322-676-1	Sequence 1, Appli
c 297	16	1.0	3877	3	US-09-466-036A-1	Sequence 1, Appli
c 298	16	1.0	3937	4	US-10-164-595-7	Sequence 7, Appli
c 299	16	1.0	3985	4	US-10-164-595-3	Sequence 3, Appli
300	16	1.0	4176	4	US-09-106-568E-1	Sequence 1, Appli
301	16	1.0	4255	4	US-09-698-286A-8	Sequence 8, Appli
302	16	1.0	4269	4	US-09-540-236-1101	Sequence 1101, Ap
c 303	16	1.0	4391	3	US-09-207-857-1	Sequence 1, Appli
c 304	16	1.0	4391	4	US-09-909-280A-1	Sequence 1, Appli
c 305	16	1.0	4528	4	US-08-809-254A-6	Sequence 6, Appli
c 306	16	1.0	4899	4	US-09-799-451-714	Sequence 714, App
c 307	16	1.0	4920	4	US-08-956-171E-26	Sequence 26, Appl
c 308	16	1.0	4920	4	US-08-781-986A-26	Sequence 26, Appl
c 309	16	1.0	4931	4	US-09-809-665A-102	Sequence 102, App
310	16	1.0	5009	4	US-09-106-568E-5	Sequence 5, Appli
c 311	16	1.0	5078	4	US-09-620-312D-565	Sequence 565, App
c 312	16	1.0	5171	4	US-08-956-171E-264	Sequence 264, App
c 313	16	1.0	5171	4	US-08-781-986A-264	Sequence 264, App
314	16	1.0	5304	4	US-09-583-110-1314	Sequence 1314, Ap
315	16	1.0	5672	4	US-09-023-655-1392	Sequence 1392, Ap
c 316	16	1.0	5935	3	US-09-178-973B-17	Sequence 17, Appl
c 317	16	1.0	5935	3	US-09-419-568F-29	Sequence 29, Appl
c 318	16	1.0	5935	3	US-09-354-243B-29	Sequence 29, Appl
319	16	1.0	6415	4	US-08-961-527-162	Sequence 162, App
c 320	16	1.0	6422	4	US-09-976-594-715	Sequence 715, App
321	16	1.0	6693	4	US-08-961-527-195	Sequence 195, App
c 322	16	1.0	6757	4	US-09-023-655-1087	Sequence 1087, Ap
c 323	16	1.0	6876	4	US-09-809-665A-15	Sequence 15, Appl
324	16	1.0	7152	3	US-09-167-681-29	Sequence 29, Appl
c 325	16	1.0	7445	3	US-09-178-973B-8	Sequence 8, Appli
c 326	16	1.0	7445	3	US-09-419-568F-8	Sequence 8, Appli
c 327	16	1.0	7445	3	US-09-354-243B-8	Sequence 8, Appli
328	16	1.0	8224	2	US-09-010-398-14	Sequence 14, Appl
329	16	1.0	8224	3	US-09-366-260-14	Sequence 14, Appl
330	16	1.0	8722	4	US-09-221-017B-263	Sequence 263, App
331	16	1.0	9997	1	US-08-246-982A-15	Sequence 15, Appl
332	16	1.0	9997	1	US-08-453-265-15	Sequence 15, Appl
333	16	1.0	10103	2	US-08-457-273B-7	Sequence 7, Appli
334	16	1.0	10348	2	US-08-457-273B-41	Sequence 41, Appl
335	16	1.0	10348	3	US-08-556-419-13	Sequence 13, Appl
336	16	1.0	10348	3	US-09-041-886-14	Sequence 14, Appl
337	16	1.0	10366	1	US-08-246-982A-5	Sequence 5, Appli
338	16	1.0	10366	1	US-08-453-265-5	Sequence 5, Appli
339	16	1.0	10711	4	US-08-961-527-145	Sequence 145, App
340	16	1.0	10862	3	US-09-058-411-1	Sequence 1, Appli
341	16	1.0	10862	4	US-09-705-949-1	Sequence 1, Appli
342	16	1.0	10892	4	US-09-452-638-52	Sequence 52, Appl
c 343	16	1.0	17327	1	US-07-906-871-15	Sequence 15, Appl
c 344	16	1.0	20284	4	US-09-526-193A-21	Sequence 21, Appl
345	16	1.0	26850	4	US-10-327-189-41	Sequence 41, Appl
346	16	1.0	28001	4	US-09-819-993-3	Sequence 3, Appli
347	16	1.0	28001	4	US-10-193-295-3	Sequence 3, Appli
c 348	16	1.0	30549	3	US-09-134-001C-322	Sequence 322, App
349	16	1.0	31063	4	US-09-596-002-20	Sequence 20, Appl
350	16	1.0	31208	4	US-09-852-067-3	Sequence 3, Appli
c 351	16	1.0	31880	3	US-09-453-702B-242	Sequence 242, App
352	16	1.0	32679	4	US-08-976-063E-1	Sequence 1, Appli
353	16	1.0	35100	1	US-08-306-691B-19	Sequence 19, Appl
354	16	1.0	35100	5	PCT-US93-06251-19	Sequence 19, Appl
c 355	16	1.0	39982	4	US-09-820-924-3	Sequence 3, Appli
c 356	16	1.0	39982	4	US-10-369-626-3	Sequence 3, Appli
357	16	1.0	40352	3	US-08-846-111D-15	Sequence 15, Appl
358	16	1.0	40352	3	US-09-443-077-15	Sequence 15, Appl
359	16	1.0	53500	4	US-09-266-965-76	Sequence 76, Appl
c 360	16	1.0	54550	4	US-10-327-189-42	Sequence 42, Appl
361	16	1.0	54945	4	US-09-967-669-10	Sequence 10, Appl
c 362	16	1.0	74962	4	US-09-685-853A-3	Sequence 3, Appli
363	16	1.0	106746	4	US-09-326-402C-1	Sequence 1, Appli
364	16	1.0	106746	4	US-09-326-402C-12	Sequence 12, Appl
365	16	1.0	114793	4	US-10-148-806-3	Sequence 3, Appli
c 366	16	1.0	254366	4	US-09-822-871-3	Sequence 3, Appli
c 367	16	1.0	392000	4	US-10-027-983-11	Sequence 11, Appl
368	16	1.0	536165	4	US-09-214-808-1	Sequence 1, Appli
c 369	16	1.0	536165	4	US-09-214-808-1	Sequence 1, Appli
370	16	1.0	580073	4	US-08-545-528D-1	Sequence 1, Appli
c 371	16	1.0	640681	4	US-09-790-988-1	Sequence 1, Appli
372	16	1.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
c 373	16	1.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
374	16	1.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
375	16	1.0	1664976	4	US-09-692-570-1	Sequence 1, Appli
376	16	1.0	1830121	4	US-09-557-884-1	Sequence 1, Appli
377	16	1.0	1830121	4	US-09-643-990A-1	Sequence 1, Appli
378	16	1.0	1830121	4	US-10-329-960-1	Sequence 1, Appli
c 379	16	1.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 380	16	1.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
381	15	0.9	18	4	US-09-422-978-4783	Sequence 4783, Ap
382	15	0.9	30	3	US-09-180-100-6	Sequence 6, Appli
383	15	0.9	33	3	US-08-454-928-3	Sequence 3, Appli
384	15	0.9	49	4	US-09-104-067-1	Sequence 1, Appli
385	15	0.9	51	4	US-09-443-199C-501	Sequence 501, App
386	15	0.9	52	4	US-09-104-067-6	Sequence 6, Appli
c 387	15	0.9	57	4	US-09-168-947-32	Sequence 32, Appl
388	15	0.9	73	4	US-09-513-999C-15343	Sequence 15343, A
c 389	15	0.9	75	4	US-09-168-947-34	Sequence 34, Appl
390	15	0.9	82	3	US-09-414-828A-10	Sequence 10, Appl
391	15	0.9	126	1	US-08-480-884-9	Sequence 9, Appli
392	15	0.9	126	5	PCT-US94-08024-9	Sequence 9, Appli

393	15	0.9	160	4	US-09-513-999C-12383	Sequence 12383, A
394	15	0.9	174	4	US-09-513-999C-31796	Sequence 31796, A
c 395	15	0.9	186	4	US-09-248-796A-13139	Sequence 13139, A
c 396	15	0.9	192	4	US-09-107-532A-2041	Sequence 2041, Ap
397	15	0.9	195	4	US-09-270-767-26579	Sequence 26579, A
398	15	0.9	195	4	US-09-248-796A-9211	Sequence 9211, Ap
c 399	15	0.9	207	4	US-09-583-110-360	Sequence 360, App
c 400	15	0.9	207	4	US-09-513-999C-16168	Sequence 16168, A
c 401	15	0.9	212	4	US-09-016-434-50	Sequence 50, Appl
c 402	15	0.9	213	4	US-09-248-796A-8081	Sequence 8081, Ap
c 403	15	0.9	216	4	US-09-248-796A-11498	Sequence 11498, A
c 404	15	0.9	222	4	US-09-248-796A-10858	Sequence 10858, A
c 405	15	0.9	223	4	US-09-513-999C-18951	Sequence 18951, A
406	15	0.9	234	4	US-09-248-796A-2960	Sequence 2960, Ap
407	15	0.9	246	4	US-09-583-110-359	Sequence 359, App
c 408	15	0.9	252	3	US-08-905-223-84	Sequence 84, Appl
409	15	0.9	253	4	US-09-513-999C-24560	Sequence 24560, A
c 410	15	0.9	258	4	US-09-248-796A-7591	Sequence 7591, Ap
411	15	0.9	261	4	US-09-248-796A-12391	Sequence 12391, A
c 412	15	0.9	264	2	US-08-774-025A-2	Sequence 2, Appli
c 413	15	0.9	264	3	US-09-244-093-2	Sequence 2, Appli
c 414	15	0.9	264	4	US-09-016-434-93	Sequence 93, Appl
c 415	15	0.9	264	4	US-09-619-758-2	Sequence 2, Appli
c 416	15	0.9	264	4	US-09-886-607-2	Sequence 2, Appli
c 417	15	0.9	264	4	US-09-270-767-7357	Sequence 7357, Ap
c 418	15	0.9	264	4	US-09-270-767-22639	Sequence 22639, A
419	15	0.9	267	4	US-09-107-532A-570	Sequence 570, App
c 420	15	0.9	276	4	US-09-023-655-82	Sequence 82, Appl
421	15	0.9	278	4	US-09-313-294A-6317	Sequence 6317, Ap
422	15	0.9	278	4	US-09-313-294A-6427	Sequence 6427, Ap
c 423	15	0.9	284	4	US-09-313-294A-3945	Sequence 3945, Ap
c 424	15	0.9	287	4	US-09-313-294A-2011	Sequence 2011, Ap
425	15	0.9	291	4	US-09-489-039A-1696	Sequence 1696, Ap
426	15	0.9	291	4	US-09-134-000C-183	Sequence 183, App
427	15	0.9	291	4	US-09-248-796A-10407	Sequence 10407, A
428	15	0.9	299	4	US-09-313-294A-6626	Sequence 6626, Ap
429	15	0.9	312	4	US-09-489-039A-465	Sequence 465, App
430	15	0.9	313	4	US-09-513-999C-24774	Sequence 24774, A
c 431	15	0.9	333	4	US-09-313-294A-3924	Sequence 3924, Ap
c 432	15	0.9	345	4	US-09-107-532A-1178	Sequence 1178, Ap
c 433	15	0.9	347	2	US-08-546-117-7	Sequence 7, Appli
c 434	15	0.9	348	4	US-09-270-767-26920	Sequence 26920, A
435	15	0.9	353	4	US-09-513-999C-15687	Sequence 15687, A
c 436	15	0.9	369	4	US-09-248-796A-8006	Sequence 8006, Ap
437	15	0.9	374	4	US-09-513-999C-11764	Sequence 11764, A
438	15	0.9	374	4	US-09-513-999C-17653	Sequence 17653, A
439	15	0.9	376	4	US-09-621-976-16394	Sequence 16394, A
440	15	0.9	384	4	US-09-107-532A-3130	Sequence 3130, Ap
c 441	15	0.9	387	4	US-09-270-767-28221	Sequence 28221, A
c 442	15	0.9	400	4	US-08-956-171E-848	Sequence 848, App
443	15	0.9	400	4	US-08-956-171E-3744	Sequence 3744, Ap
c 444	15	0.9	400	4	US-08-781-986A-848	Sequence 848, App
445	15	0.9	400	4	US-08-781-986A-3744	Sequence 3744, Ap
c 446	15	0.9	405	4	US-09-495-050A-213	Sequence 213, App
447	15	0.9	405	4	US-09-134-000C-744	Sequence 744, App
448	15	0.9	406	4	US-09-621-976-16393	Sequence 16393, A
c 449	15	0.9	408	4	US-09-248-796A-7532	Sequence 7532, Ap
c 450	15	0.9	409	4	US-09-513-999C-31382	Sequence 31382, A
c 451	15	0.9	414	4	US-09-134-000C-2784	Sequence 2784, Ap
c 452	15	0.9	415	1	US-08-612-890-2	Sequence 2, Appli
453	15	0.9	416	4	US-09-497-491-22	Sequence 22, Appl
454	15	0.9	417	4	US-09-513-999C-10080	Sequence 10080, A
455	15	0.9	421	4	US-09-497-491-28	Sequence 28, Appl
c 456	15	0.9	432	4	US-09-621-976-2133	Sequence 2133, Ap
457	15	0.9	440	4	US-09-513-999C-12746	Sequence 12746, A
c 458	15	0.9	458	4	US-09-270-767-12454	Sequence 12454, A
459	15	0.9	461	4	US-09-270-767-3991	Sequence 3991, Ap
460	15	0.9	461	4	US-09-270-767-19273	Sequence 19273, A
461	15	0.9	462	4	US-09-621-976-17620	Sequence 17620, A
462	15	0.9	468	4	US-09-248-796A-10273	Sequence 10273, A
463	15	0.9	474	4	US-09-446-880A-3	Sequence 3, Appli
464	15	0.9	478	4	US-09-621-976-1741	Sequence 1741, Ap
c 465	15	0.9	480	4	US-09-543-681A-2611	Sequence 2611, Ap
c 466	15	0.9	483	1	US-08-644-664B-8	Sequence 8, Appli
c 467	15	0.9	483	2	US-08-761-277A-8	Sequence 8, Appli
c 468	15	0.9	483	2	US-08-715-808-15	Sequence 15, Appl
469	15	0.9	483	4	US-09-621-976-17538	Sequence 17538, A
470	15	0.9	483	4	US-09-270-767-12964	Sequence 12964, A
c 471	15	0.9	501	4	US-09-543-681A-1522	Sequence 1522, Ap
c 472	15	0.9	501	4	US-09-248-796A-2397	Sequence 2397, Ap
c 473	15	0.9	501	4	US-09-248-796A-2400	Sequence 2400, Ap
474	15	0.9	504	4	US-09-252-991A-4925	Sequence 4925, Ap
c 475	15	0.9	504	4	US-09-248-796A-1506	Sequence 1506, Ap
476	15	0.9	510	4	US-09-621-976-840	Sequence 840, App
477	15	0.9	514	4	US-09-621-976-145	Sequence 145, App
478	15	0.9	519	4	US-09-621-976-16272	Sequence 16272, A
479	15	0.9	525	4	US-09-248-796A-5196	Sequence 5196, Ap
480	15	0.9	526	4	US-09-513-999C-13232	Sequence 13232, A
c 481	15	0.9	538	4	US-09-621-976-14167	Sequence 14167, A
482	15	0.9	540	1	US-07-990-965-1	Sequence 1, Appli
c 483	15	0.9	540	4	US-09-252-991A-13817	Sequence 13817, A
484	15	0.9	540	4	US-09-270-767-8393	Sequence 8393, Ap
485	15	0.9	540	4	US-09-270-767-23675	Sequence 23675, A
c 486	15	0.9	543	4	US-09-252-991A-1929	Sequence 1929, Ap
c 487	15	0.9	550	4	US-09-306-420C-17	Sequence 17, Appl
c 488	15	0.9	550	4	US-09-306-420C-19	Sequence 19, Appl
489	15	0.9	554	4	US-09-513-999C-1718	Sequence 1718, Ap
c 490	15	0.9	556	4	US-09-621-976-16098	Sequence 16098, A
c 491	15	0.9	558	4	US-09-252-991A-7770	Sequence 7770, Ap
492	15	0.9	562	4	US-09-513-999C-8342	Sequence 8342, Ap
c 493	15	0.9	568	3	US-08-998-416-1109	Sequence 1109, Ap
c 494	15	0.9	572	4	US-09-621-976-16094	Sequence 16094, A
495	15	0.9	572	4	US-09-270-767-7847	Sequence 7847, Ap
496	15	0.9	572	4	US-09-270-767-23129	Sequence 23129, A
c 497	15	0.9	574	1	US-08-612-890-1	Sequence 1, Appli
c 498	15	0.9	583	6	5225348-8	Patent No. 5225348
c 499	15	0.9	584	4	US-09-270-391-24	Sequence 24, Appl
c 500	15	0.9	585	3	US-08-075-520A-27	Sequence 27, Appl
c 501	15	0.9	588	4	US-09-710-279-2119	Sequence 2119, Ap
502	15	0.9	589	4	US-09-621-976-17537	Sequence 17537, A
c 503	15	0.9	599	6	5225348-9	Patent No. 5225348
c 504	15	0.9	600	4	US-09-489-039A-4150	Sequence 4150, Ap
505	15	0.9	606	4	US-09-248-796A-4562	Sequence 4562, Ap
506	15	0.9	606	4	US-09-248-796A-4806	Sequence 4806, Ap
c 507	15	0.9	612	4	US-09-248-796A-9210	Sequence 9210, Ap
c 508	15	0.9	613	4	US-09-497-855A-13	Sequence 13, Appl
c 509	15	0.9	613	4	US-09-270-767-2331	Sequence 2331, Ap
c 510	15	0.9	613	4	US-09-270-767-17613	Sequence 17613, A
511	15	0.9	617	4	US-09-221-017B-321	Sequence 321, App
512	15	0.9	618	3	US-09-385-982-59	Sequence 59, Appl
513	15	0.9	618	4	US-09-543-681A-316	Sequence 316, App
c 514	15	0.9	624	3	US-08-884-077-5	Sequence 5, Appli
c 515	15	0.9	627	3	US-09-134-001C-2763	Sequence 2763, Ap
c 516	15	0.9	630	4	US-09-489-039A-1859	Sequence 1859, Ap
c 517	15	0.9	636	4	US-09-134-000C-2081	Sequence 2081, Ap
518	15	0.9	638	3	US-09-328-111-26	Sequence 26, Appl
c 519	15	0.9	639	4	US-09-248-796A-1157	Sequence 1157, Ap
c 520	15	0.9	644	4	US-09-270-767-5869	Sequence 5869, Ap
c 521	15	0.9	644	4	US-09-270-767-21151	Sequence 21151, A
c 522	15	0.9	645	4	US-09-543-681A-428	Sequence 428, App
523	15	0.9	651	4	US-09-328-352-350	Sequence 350, App
c 524	15	0.9	666	4	US-09-107-532A-3649	Sequence 3649, Ap
c 525	15	0.9	668	3	US-08-578-634C-2	Sequence 2, Appli
c 526	15	0.9	668	3	US-09-430-010-2	Sequence 2, Appli
527	15	0.9	669	3	US-08-928-941D-23	Sequence 23, Appl
528	15	0.9	669	3	US-09-280-590A-23	Sequence 23, Appl
529	15	0.9	669	4	US-09-892-398-23	Sequence 23, Appl
530	15	0.9	672	4	US-09-543-681A-1954	Sequence 1954, Ap
531	15	0.9	673	4	US-09-270-767-7515	Sequence 7515, Ap
532	15	0.9	673	4	US-09-270-767-22797	Sequence 22797, A
c 533	15	0.9	681	4	US-09-471-573A-1	Sequence 1, Appli
c 534	15	0.9	708	4	US-09-328-352-2733	Sequence 2733, Ap
535	15	0.9	712	4	US-09-621-976-1814	Sequence 1814, Ap
c 536	15	0.9	712	4	US-09-270-767-13279	Sequence 13279, A
537	15	0.9	716	3	US-08-998-416-945	Sequence 945, App
c 538	15	0.9	717	4	US-09-107-532A-548	Sequence 548, App

539	15	0.9	729	4	US-09-328-352-792	Sequence 792, App
540	15	0.9	732	4	US-09-601-198-112	Sequence 112, App
541	15	0.9	735	4	US-09-328-352-3768	Sequence 3768, Ap
c 542	15	0.9	747	4	US-09-583-110-1445	Sequence 1445, Ap
543	15	0.9	753	3	US-09-134-001C-1562	Sequence 1562, Ap
544	15	0.9	756	4	US-09-252-991A-2114	Sequence 2114, Ap
545	15	0.9	759	4	US-09-134-000C-1071	Sequence 1071, Ap
546	15	0.9	759	4	US-09-248-796A-143	Sequence 143, App
547	15	0.9	762	4	US-09-248-796A-2906	Sequence 2906, Ap
c 548	15	0.9	780	4	US-09-134-000C-1237	Sequence 1237, Ap
c 549	15	0.9	786	4	US-09-543-681A-3016	Sequence 3016, Ap
550	15	0.9	787	1	US-08-236-427-12	Sequence 12, Appl
551	15	0.9	791	3	US-08-858-207A-231	Sequence 231, App
c 552	15	0.9	795	4	US-09-489-039A-1961	Sequence 1961, Ap
553	15	0.9	798	2	US-08-319-866-7	Sequence 7, Appli
554	15	0.9	798	4	US-08-809-917-7	Sequence 7, Appli
c 555	15	0.9	801	4	US-09-489-039A-646	Sequence 646, App
556	15	0.9	803	3	US-08-454-928-9	Sequence 9, Appli
557	15	0.9	806	4	US-09-270-767-9377	Sequence 9377, Ap
558	15	0.9	806	4	US-09-270-767-24659	Sequence 24659, A
559	15	0.9	807	4	US-09-248-796A-3765	Sequence 3765, Ap
c 560	15	0.9	808	4	US-09-328-475C-109	Sequence 109, App
c 561	15	0.9	817	1	US-08-378-011A-4	Sequence 4, Appli
562	15	0.9	825	4	US-09-543-681A-2474	Sequence 2474, Ap
c 563	15	0.9	831	3	US-09-342-681C-10	Sequence 10, Appl
c 564	15	0.9	845	1	US-08-378-011A-2	Sequence 2, Appli
c 565	15	0.9	846	4	US-09-247-890-9	Sequence 9, Appli
c 566	15	0.9	846	4	US-09-724-969-9	Sequence 9, Appli
c 567	15	0.9	846	4	US-09-724-852-9	Sequence 9, Appli
c 568	15	0.9	846	6	5164485-1	Patent No. 5164485
569	15	0.9	849	4	US-09-328-352-2632	Sequence 2632, Ap
c 570	15	0.9	855	3	US-09-247-373B-37	Sequence 37, Appl
c 571	15	0.9	855	4	US-09-270-767-11359	Sequence 11359, A
572	15	0.9	871	5	PCT-US91-06234A-7	Sequence 7, Appli
573	15	0.9	876	3	US-09-167-513-1	Sequence 1, Appli
574	15	0.9	885	4	US-09-252-991A-7716	Sequence 7716, Ap
575	15	0.9	885	4	US-09-328-352-3427	Sequence 3427, Ap
c 576	15	0.9	893	2	US-08-500-914A-1	Sequence 1, Appli
577	15	0.9	900	1	US-07-990-965-4	Sequence 4, Appli
c 578	15	0.9	900	4	US-09-583-110-330	Sequence 330, App
c 579	15	0.9	900	4	US-09-861-451A-41	Sequence 41, Appl
580	15	0.9	909	4	US-09-252-991A-5120	Sequence 5120, Ap
581	15	0.9	909	4	US-09-328-352-1880	Sequence 1880, Ap
582	15	0.9	912	4	US-09-248-796A-2401	Sequence 2401, Ap
583	15	0.9	913	4	US-09-702-114A-1	Sequence 1, Appli
c 584	15	0.9	918	4	US-09-107-532A-2868	Sequence 2868, Ap
c 585	15	0.9	918	4	US-09-107-532A-2870	Sequence 2870, Ap
c 586	15	0.9	918	4	US-09-107-532A-2871	Sequence 2871, Ap
c 587	15	0.9	918	4	US-09-107-532A-2873	Sequence 2873, Ap
c 588	15	0.9	918	4	US-09-107-532A-2875	Sequence 2875, Ap
c 589	15	0.9	918	4	US-09-107-532A-2877	Sequence 2877, Ap
590	15	0.9	921	4	US-09-011-143-6	Sequence 6, Appli
591	15	0.9	921	4	US-09-011-143-7	Sequence 7, Appli
592	15	0.9	921	4	US-09-302-495-6	Sequence 6, Appli
593	15	0.9	921	4	US-09-302-495-7	Sequence 7, Appli
594	15	0.9	921	4	US-10-079-616-6	Sequence 6, Appli
595	15	0.9	921	4	US-10-079-616-7	Sequence 7, Appli
c 596	15	0.9	932	4	US-09-526-597D-1	Sequence 1, Appli
c 597	15	0.9	933	4	US-09-107-532A-78	Sequence 78, Appl
c 598	15	0.9	933	4	US-09-107-532A-531	Sequence 531, App
c 599	15	0.9	936	4	US-09-107-532A-3111	Sequence 3111, Ap
c 600	15	0.9	943	1	US-07-807-043B-12	Sequence 12, Appl
c 601	15	0.9	943	1	US-08-299-849B-12	Sequence 12, Appl
c 602	15	0.9	943	2	US-08-142-368A-12	Sequence 12, Appl
c 603	15	0.9	943	3	US-08-967-727-12	Sequence 12, Appl
c 604	15	0.9	943	3	US-08-037-230D-12	Sequence 12, Appl
c 605	15	0.9	943	4	US-09-583-850-12	Sequence 12, Appl
c 606	15	0.9	943	4	US-09-579-197-12	Sequence 12, Appl
c 607	15	0.9	943	4	US-09-404-026-12	Sequence 12, Appl
c 608	15	0.9	943	4	US-09-312-464-12	Sequence 12, Appl
c 609	15	0.9	945	3	US-09-056-105-7	Sequence 7, Appli
c 610	15	0.9	945	4	US-09-392-714-19	Sequence 19, Appl
611	15	0.9	948	3	US-09-247-155-50	Sequence 50, Appl
612	15	0.9	948	4	US-09-599-360B-13	Sequence 13, Appl
613	15	0.9	950	4	US-09-270-767-8142	Sequence 8142, Ap
614	15	0.9	950	4	US-09-270-767-23424	Sequence 23424, A
615	15	0.9	957	4	US-09-866-028-90	Sequence 90, Appl
616	15	0.9	957	4	US-09-944-457-90	Sequence 90, Appl
617	15	0.9	963	4	US-10-140-002-389	Sequence 389, App
c 618	15	0.9	978	4	US-09-134-000C-2710	Sequence 2710, Ap
619	15	0.9	984	4	US-09-248-796A-968	Sequence 968, App
620	15	0.9	987	1	US-08-186-529-1	Sequence 1, Appli
621	15	0.9	987	1	US-08-640-386A-1	Sequence 1, Appli
622	15	0.9	987	3	US-08-848-760B-24	Sequence 24, Appl
623	15	0.9	987	4	US-09-489-039A-1978	Sequence 1978, Ap
624	15	0.9	987	4	US-09-826-025-24	Sequence 24, Appl
625	15	0.9	990	3	US-09-079-984A-1	Sequence 1, Appli
626	15	0.9	990	3	US-09-079-984A-11	Sequence 11, Appl
627	15	0.9	990	4	US-09-390-729-1	Sequence 1, Appli
628	15	0.9	990	4	US-09-390-729-11	Sequence 11, Appl
629	15	0.9	993	4	US-09-328-352-2754	Sequence 2754, Ap
630	15	0.9	999	4	US-09-328-352-709	Sequence 709, App
c 631	15	0.9	1008	4	US-09-489-039A-3748	Sequence 3748, Ap
632	15	0.9	1008	4	US-09-583-110-1297	Sequence 1297, Ap
633	15	0.9	1017	4	US-09-270-767-13274	Sequence 13274, A
634	15	0.9	1018	2	US-08-184-009-194	Sequence 194, App
635	15	0.9	1018	2	US-08-458-356-194	Sequence 194, App
636	15	0.9	1018	3	US-08-460-736-194	Sequence 194, App
637	15	0.9	1018	4	US-09-535-370-194	Sequence 194, App
638	15	0.9	1018	4	US-09-663-667-194	Sequence 194, App
c 639	15	0.9	1019	3	US-09-056-105-13	Sequence 13, Appl
c 640	15	0.9	1019	4	US-09-270-767-9786	Sequence 9786, Ap
c 641	15	0.9	1019	4	US-09-270-767-25068	Sequence 25068, A
642	15	0.9	1020	4	US-09-107-532A-3293	Sequence 3293, Ap
643	15	0.9	1022	3	US-09-222-575-67	Sequence 67, Appl
644	15	0.9	1022	4	US-09-389-681-67	Sequence 67, Appl
645	15	0.9	1022	4	US-09-620-405B-67	Sequence 67, Appl
646	15	0.9	1022	4	US-09-339-338-67	Sequence 67, Appl
647	15	0.9	1022	4	US-09-433-826B-67	Sequence 67, Appl
648	15	0.9	1022	4	US-09-604-287A-67	Sequence 67, Appl
649	15	0.9	1022	4	US-09-285-480-67	Sequence 67, Appl
650	15	0.9	1022	4	US-09-834-759-67	Sequence 67, Appl
651	15	0.9	1022	4	US-09-590-751A-67	Sequence 67, Appl
c 652	15	0.9	1024	4	US-09-328-475C-65	Sequence 65, Appl
653	15	0.9	1026	4	US-09-489-039A-5619	Sequence 5619, Ap
654	15	0.9	1037	3	US-08-858-207A-149	Sequence 149, App
c 655	15	0.9	1040	4	US-09-023-655-1487	Sequence 1487, Ap
c 656	15	0.9	1047	4	US-09-252-991A-5002	Sequence 5002, Ap
657	15	0.9	1062	4	US-09-248-796A-10507	Sequence 10507, A
658	15	0.9	1068	4	US-09-170-496D-1	Sequence 1, Appli
659	15	0.9	1068	4	US-09-170-496D-163	Sequence 163, App
c 660	15	0.9	1068	4	US-09-328-352-996	Sequence 996, App
c 661	15	0.9	1095	4	US-09-248-796A-11826	Sequence 11826, A
c 662	15	0.9	1098	4	US-09-583-110-437	Sequence 437, App
663	15	0.9	1116	3	US-08-928-941D-17	Sequence 17, Appl
664	15	0.9	1116	3	US-09-280-590A-17	Sequence 17, Appl
665	15	0.9	1116	4	US-09-892-398-17	Sequence 17, Appl
666	15	0.9	1128	4	US-09-205-258-182	Sequence 182, App
c 667	15	0.9	1134	4	US-09-248-796A-6128	Sequence 6128, Ap
668	15	0.9	1149	4	US-09-970-516-5	Sequence 5, Appli
c 669	15	0.9	1149	4	US-09-248-796A-3354	Sequence 3354, Ap
c 670	15	0.9	1164	4	US-09-489-039A-1222	Sequence 1222, Ap
c 671	15	0.9	1167	4	US-09-583-110-704	Sequence 704, App
c 672	15	0.9	1178	4	US-09-270-767-26116	Sequence 26116, A
673	15	0.9	1182	4	US-09-252-991A-13631	Sequence 13631, A
674	15	0.9	1183	4	US-09-799-451-203	Sequence 203, App
c 675	15	0.9	1185	1	US-07-757-536B-5	Sequence 5, Appli
c 676	15	0.9	1188	4	US-09-328-352-1693	Sequence 1693, Ap
c 677	15	0.9	1189	1	US-07-757-536B-4	Sequence 4, Appli
c 678	15	0.9	1200	3	US-08-854-531-5	Sequence 5, Appli
679	15	0.9	1200	4	US-09-107-532A-1060	Sequence 1060, Ap
c 680	15	0.9	1200	5	PCT-US95-13552-5	Sequence 5, Appli
681	15	0.9	1203	4	US-09-134-000C-2824	Sequence 2824, Ap
c 682	15	0.9	1208	4	US-09-461-325-14	Sequence 14, Appl
c 683	15	0.9	1208	4	US-10-012-542-14	Sequence 14, Appl
c 684	15	0.9	1208	4	US-10-115-123-14	Sequence 14, Appl

	685	15	0.9	1227	4	US-09-602-787A-115	Sequence 115, App
c	686	15	0.9	1230	3	US-08-890-719-8	Sequence 8, Appli
c	687	15	0.9	1230	3	US-09-134-001C-953	Sequence 953, App
	688	15	0.9	1233	4	US-09-270-767-4229	Sequence 4229, Ap
	689	15	0.9	1233	4	US-09-270-767-19511	Sequence 19511, A
	690	15	0.9	1248	4	US-09-774-528-119	Sequence 119, App
	691	15	0.9	1260	4	US-09-583-110-2466	Sequence 2466, Ap
	692	15	0.9	1266	4	US-10-140-002-319	Sequence 319, App
c	693	15	0.9	1268	4	US-09-484-970B-86	Sequence 86, Appl
	694	15	0.9	1272	2	US-08-972-258-1	Sequence 1, Appli
	695	15	0.9	1272	3	US-09-263-128-1	Sequence 1, Appli
	696	15	0.9	1272	4	US-09-641-111A-1	Sequence 1, Appli
	697	15	0.9	1277	4	US-09-620-312D-968	Sequence 968, App
c	698	15	0.9	1281	4	US-09-489-039A-1380	Sequence 1380, Ap
c	699	15	0.9	1283	4	US-09-976-594-58	Sequence 58, Appl
c	700	15	0.9	1284	4	US-09-489-039A-1322	Sequence 1322, Ap
	701	15	0.9	1284	4	US-09-248-796A-2331	Sequence 2331, Ap
	702	15	0.9	1285	4	US-09-023-655-333	Sequence 333, App
c	703	15	0.9	1286	4	US-10-133-907-3	Sequence 3, Appli
c	704	15	0.9	1287	4	US-09-248-796A-731	Sequence 731, App
	705	15	0.9	1293	3	US-09-182-145-13	Sequence 13, Appl
c	706	15	0.9	1293	3	US-09-182-145-14	Sequence 14, Appl
c	707	15	0.9	1299	4	US-09-107-532A-1666	Sequence 1666, Ap
	708	15	0.9	1308	4	US-09-248-796A-927	Sequence 927, App
	709	15	0.9	1313	1	US-08-176-427B-7	Sequence 7, Appli
	710	15	0.9	1313	2	US-08-356-060A-4	Sequence 4, Appli
	711	15	0.9	1313	3	US-08-460-900C-4	Sequence 4, Appli
	712	15	0.9	1313	3	US-08-674-509B-4	Sequence 4, Appli
	713	15	0.9	1313	3	US-08-954-698-4	Sequence 4, Appli
	714	15	0.9	1313	3	US-08-957-874-4	Sequence 4, Appli
	715	15	0.9	1313	4	US-09-325-256-8	Sequence 8, Appli
	716	15	0.9	1313	4	US-09-639-695-4	Sequence 4, Appli
	717	15	0.9	1313	4	US-09-448-188-4	Sequence 4, Appli
	718	15	0.9	1313	4	US-08-954-128-4	Sequence 4, Appli
	719	15	0.9	1313	4	US-09-704-917-4	Sequence 4, Appli
	720	15	0.9	1313	4	US-08-954-740-4	Sequence 4, Appli
	721	15	0.9	1313	4	US-09-151-999-4	Sequence 4, Appli
	722	15	0.9	1313	4	US-09-736-476-4	Sequence 4, Appli
	723	15	0.9	1313	4	US-09-418-221-4	Sequence 4, Appli
	724	15	0.9	1314	3	US-09-057-860A-5	Sequence 5, Appli
	725	15	0.9	1314	4	US-09-021-660A-30	Sequence 30, Appl
	726	15	0.9	1317	4	US-09-107-532A-110	Sequence 110, App
	727	15	0.9	1329	2	US-08-758-621-1	Sequence 1, Appli
	728	15	0.9	1329	3	US-09-107-858-1	Sequence 1, Appli
	729	15	0.9	1329	4	US-09-579-174-1	Sequence 1, Appli
c	730	15	0.9	1332	4	US-09-252-991A-1642	Sequence 1642, Ap
	731	15	0.9	1332	4	US-09-252-991A-1946	Sequence 1946, Ap
	732	15	0.9	1335	3	US-08-954-536-15	Sequence 15, Appl
c	733	15	0.9	1335	4	US-09-248-796A-5070	Sequence 5070, Ap
	734	15	0.9	1344	1	US-07-940-852-1	Sequence 1, Appli
	735	15	0.9	1344	1	US-08-396-126-1	Sequence 1, Appli
	736	15	0.9	1353	4	US-09-809-665A-27	Sequence 27, Appl
c	737	15	0.9	1356	4	US-09-705-621-34	Sequence 34, Appl
	738	15	0.9	1365	3	US-09-221-235-6	Sequence 6, Appli
	739	15	0.9	1365	3	US-09-221-928-6	Sequence 6, Appli
	740	15	0.9	1365	3	US-09-221-527-6	Sequence 6, Appli
	741	15	0.9	1365	3	US-09-221-236-6	Sequence 6, Appli
	742	15	0.9	1365	3	US-09-221-416-6	Sequence 6, Appli
	743	15	0.9	1365	3	US-09-221-245-6	Sequence 6, Appli
	744	15	0.9	1365	3	US-09-163-115-6	Sequence 6, Appli
	745	15	0.9	1365	3	US-09-221-528-6	Sequence 6, Appli
	746	15	0.9	1365	3	US-09-593-553-6	Sequence 6, Appli
	747	15	0.9	1365	3	US-09-221-237-6	Sequence 6, Appli
	748	15	0.9	1365	4	US-09-757-982-6	Sequence 6, Appli
c	749	15	0.9	1375	2	US-08-993-738A-2	Sequence 2, Appli
c	750	15	0.9	1375	3	US-08-713-354C-2	Sequence 2, Appli
c	751	15	0.9	1375	3	US-09-241-268-2	Sequence 2, Appli
c	752	15	0.9	1375	4	US-09-495-562-2	Sequence 2, Appli
	753	15	0.9	1378	5	PCT-US93-08479-3	Sequence 3, Appli
c	754	15	0.9	1382	5	PCT-US92-07982A-1	Sequence 1, Appli
c	755	15	0.9	1388	4	US-09-270-767-10669	Sequence 10669, A
	756	15	0.9	1389	4	US-09-634-368-4	Sequence 4, Appli
	757	15	0.9	1392	4	US-09-252-991A-13431	Sequence 13431, A
c	758	15	0.9	1393	1	US-08-174-467-18	Sequence 18, Appl
c	759	15	0.9	1393	3	US-08-452-071-18	Sequence 18, Appl
	760	15	0.9	1399	2	US-08-751-767A-3	Sequence 3, Appli
	761	15	0.9	1416	4	US-09-107-532A-1086	Sequence 1086, Ap
c	762	15	0.9	1420	1	US-08-358-171-1	Sequence 1, Appli
c	763	15	0.9	1420	3	US-09-090-947-1	Sequence 1, Appli
c	764	15	0.9	1431	3	US-09-078-173A-7	Sequence 7, Appli
	765	15	0.9	1431	4	US-09-107-532A-1593	Sequence 1593, Ap
c	766	15	0.9	1431	4	US-10-042-991-7	Sequence 7, Appli
c	767	15	0.9	1431	4	US-09-799-451-720	Sequence 720, App
c	768	15	0.9	1436	4	US-08-961-527-327	Sequence 327, App
	769	15	0.9	1438	4	US-09-016-434-1426	Sequence 1426, Ap
c	770	15	0.9	1440	4	US-09-270-767-1608	Sequence 1608, Ap
c	771	15	0.9	1440	4	US-09-270-767-16890	Sequence 16890, A
c	772	15	0.9	1443	3	US-09-078-173A-8	Sequence 8, Appli
c	773	15	0.9	1443	4	US-10-042-991-8	Sequence 8, Appli
c	774	15	0.9	1451	1	US-08-644-664B-11	Sequence 11, Appl
c	775	15	0.9	1451	2	US-08-761-277A-11	Sequence 11, Appl
c	776	15	0.9	1451	3	US-08-848-760B-14	Sequence 14, Appl
c	777	15	0.9	1451	4	US-09-826-025-14	Sequence 14, Appl
c	778	15	0.9	1452	3	US-09-078-173A-9	Sequence 9, Appli
c	779	15	0.9	1452	4	US-10-042-991-9	Sequence 9, Appli
c	780	15	0.9	1464	3	US-09-078-173A-27	Sequence 27, Appl
c	781	15	0.9	1464	4	US-09-248-796A-5148	Sequence 5148, Ap
c	782	15	0.9	1464	4	US-10-042-991-27	Sequence 27, Appl
c	783	15	0.9	1467	3	US-09-078-173A-10	Sequence 10, Appl
c	784	15	0.9	1467	4	US-10-042-991-10	Sequence 10, Appl
c	785	15	0.9	1479	4	US-09-543-681A-2092	Sequence 2092, Ap
c	786	15	0.9	1500	4	US-09-252-991A-4920	Sequence 4920, Ap
	787	15	0.9	1501	4	US-09-774-528-231	Sequence 231, App
c	788	15	0.9	1506	4	US-09-583-110-643	Sequence 643, App
	789	15	0.9	1512	4	US-09-252-991A-1481	Sequence 1481, Ap
c	790	15	0.9	1524	4	US-09-328-352-165	Sequence 165, App
c	791	15	0.9	1535	1	US-08-910-973-10	Sequence 10, Appl
c	792	15	0.9	1535	4	US-09-499-227-10	Sequence 10, Appl
c	793	15	0.9	1550	3	US-09-234-332-3	Sequence 3, Appli
	794	15	0.9	1551	4	US-09-248-796A-549	Sequence 549, App
c	795	15	0.9	1558	4	US-09-461-325-66	Sequence 66, Appl
c	796	15	0.9	1558	4	US-10-012-542-66	Sequence 66, Appl
c	797	15	0.9	1558	4	US-10-115-123-66	Sequence 66, Appl
	798	15	0.9	1560	2	US-08-751-767A-11	Sequence 11, Appl
c	799	15	0.9	1561	1	US-07-757-536B-1	Sequence 1, Appli
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	802	15	0.9	1576	1	US-08-689-974-2	Sequence 2, Appli
	803	15	0.9	1576	3	US-09-058-376-2	Sequence 2, Appli
	804	15	0.9	1584	4	US-09-107-532A-1924	Sequence 1924, Ap
c	805	15	0.9	1587	3	US-09-108-020-11	Sequence 11, Appl
c	806	15	0.9	1587	4	US-09-685-296-11	Sequence 11, Appl
	807	15	0.9	1605	4	US-09-710-279-919	Sequence 919, App
	808	15	0.9	1620	4	US-09-252-991A-4922	Sequence 4922, Ap
	809	15	0.9	1623	2	US-08-751-767A-9	Sequence 9, Appli
c	810	15	0.9	1626	4	US-09-248-796A-10954	Sequence 10954, A
c	811	15	0.9	1640	1	US-07-807-043B-11	Sequence 11, Appl
c	812	15	0.9	1640	1	US-08-299-849B-11	Sequence 11, Appl
c	813	15	0.9	1640	2	US-08-142-368A-11	Sequence 11, Appl
c	814	15	0.9	1640	3	US-08-967-727-11	Sequence 11, Appl
c	815	15	0.9	1640	3	US-08-037-230D-11	Sequence 11, Appl
c	816	15	0.9	1640	4	US-09-583-850-11	Sequence 11, Appl
c	817	15	0.9	1640	4	US-09-579-197-11	Sequence 11, Appl
c	818	15	0.9	1640	4	US-09-404-026-11	Sequence 11, Appl
c	819	15	0.9	1640	4	US-09-312-464-11	Sequence 11, Appl
	820	15	0.9	1641	4	US-09-107-532A-1105	Sequence 1105, Ap
	821	15	0.9	1648	3	US-09-165-241-2	Sequence 2, Appli
c	822	15	0.9	1650	4	US-09-248-796A-6751	Sequence 6751, Ap
c	823	15	0.9	1653	4	US-09-248-796A-336	Sequence 336, App
	824	15	0.9	1659	4	US-09-614-221A-234	Sequence 234, App
c	825	15	0.9	1665	4	US-09-221-017B-1017	Sequence 1017, Ap
c	826	15	0.9	1668	4	US-09-614-221A-420	Sequence 420, App
	827	15	0.9	1674	4	US-09-248-796A-10284	Sequence 10284, A
c	828	15	0.9	1695	4	US-09-107-532A-3316	Sequence 3316, Ap
c	829	15	0.9	1700	4	US-09-040-981-1	Sequence 1, Appli
c	830	15	0.9	1705	4	US-09-964-994B-6	Sequence 6, Appli

	831	15	0.9	1713	4	US-09-489-039A-4371	Sequence 4371, Ap
	832	15	0.9	1715	3	US-08-757-230A-1	Sequence 1, Appli
	833	15	0.9	1715	4	US-08-700-393-1	Sequence 1, Appli
	834	15	0.9	1715	5	PCT-US95-02315-1	Sequence 1, Appli
c	835	15	0.9	1718	4	US-09-221-268D-6	Sequence 6, Appli
c	836	15	0.9	1719	4	US-09-328-352-50	Sequence 50, Appl
	837	15	0.9	1737	4	US-09-270-767-13732	Sequence 13732, A
	838	15	0.9	1772	3	US-09-276-531-86	Sequence 86, Appl
c	839	15	0.9	1774	4	US-09-311-021-99	Sequence 99, Appl
c	840	15	0.9	1797	4	US-09-248-796A-5087	Sequence 5087, Ap
c	841	15	0.9	1839	4	US-09-248-796A-4430	Sequence 4430, Ap
	842	15	0.9	1847	3	US-08-858-207A-64	Sequence 64, Appl
c	843	15	0.9	1854	4	US-09-543-681A-200	Sequence 200, App
	844	15	0.9	1870	4	US-09-310-842-4	Sequence 4, Appli
	845	15	0.9	1875	2	US-08-683-743-3	Sequence 3, Appli
c	846	15	0.9	1893	4	US-09-583-110-2050	Sequence 2050, Ap
c	847	15	0.9	1926	4	US-09-248-796A-5825	Sequence 5825, Ap
	848	15	0.9	1929	4	US-09-543-681A-3758	Sequence 3758, Ap
c	849	15	0.9	1929	4	US-09-248-796A-1277	Sequence 1277, Ap
	850	15	0.9	1963	4	US-09-270-767-11063	Sequence 11063, A
	851	15	0.9	1982	1	US-08-480-547A-12	Sequence 12, Appl
	852	15	0.9	1982	1	US-08-250-847B-12	Sequence 12, Appl
	853	15	0.9	1982	2	US-08-463-949A-12	Sequence 12, Appl
	854	15	0.9	1982	3	US-08-464-410A-12	Sequence 12, Appl
	855	15	0.9	1982	5	PCT-US94-06066-12	Sequence 12, Appl
	856	15	0.9	1992	3	US-08-776-265-6	Sequence 6, Appli
	857	15	0.9	1992	4	US-09-398-184-6	Sequence 6, Appli
	858	15	0.9	2006	4	US-09-354-123-5	Sequence 5, Appli
	859	15	0.9	2009	4	US-09-809-665A-104	Sequence 104, App
	860	15	0.9	2024	2	US-08-458-970A-1	Sequence 1, Appli
	861	15	0.9	2031	4	US-09-252-991A-5180	Sequence 5180, Ap
	862	15	0.9	2034	4	US-09-252-991A-1531	Sequence 1531, Ap
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	864	15	0.9	2059	4	US-09-604-978-5	Sequence 5, Appli
	865	15	0.9	2059	4	US-09-604-728-5	Sequence 5, Appli
	866	15	0.9	2059	4	US-10-325-878-5	Sequence 5, Appli
	867	15	0.9	2060	1	US-08-480-547A-11	Sequence 11, Appl
	868	15	0.9	2060	1	US-08-250-847B-11	Sequence 11, Appl
	869	15	0.9	2060	2	US-08-463-949A-11	Sequence 11, Appl
	870	15	0.9	2060	3	US-08-464-410A-11	Sequence 11, Appl
	871	15	0.9	2060	5	PCT-US94-06066-11	Sequence 11, Appl
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c	873	15	0.9	2105	3	US-09-446-821A-1	Sequence 1, Appli
	874	15	0.9	2119	4	US-09-399-588-1	Sequence 1, Appli
	875	15	0.9	2120	3	US-09-221-235-4	Sequence 4, Appli
	876	15	0.9	2120	3	US-09-221-928-4	Sequence 4, Appli
	877	15	0.9	2120	3	US-09-221-527-4	Sequence 4, Appli
	878	15	0.9	2120	3	US-09-221-236-4	Sequence 4, Appli
	879	15	0.9	2120	3	US-09-221-416-4	Sequence 4, Appli
	880	15	0.9	2120	3	US-09-221-245-4	Sequence 4, Appli
	881	15	0.9	2120	3	US-09-163-115-4	Sequence 4, Appli
	882	15	0.9	2120	3	US-09-221-528-4	Sequence 4, Appli
	883	15	0.9	2120	3	US-09-593-553-4	Sequence 4, Appli
	884	15	0.9	2120	3	US-09-221-237-4	Sequence 4, Appli
	885	15	0.9	2120	4	US-09-757-982-4	Sequence 4, Appli
	886	15	0.9	2122	4	US-09-710-279-4457	Sequence 4457, Ap
	887	15	0.9	2166	4	US-09-134-000C-2061	Sequence 2061, Ap
	888	15	0.9	2170	4	US-09-854-133-728	Sequence 728, App
	889	15	0.9	2180	3	US-09-269-731-5	Sequence 5, Appli
c	890	15	0.9	2181	4	US-09-583-110-121	Sequence 121, App
	891	15	0.9	2193	4	US-09-011-143-5	Sequence 5, Appli
	892	15	0.9	2193	4	US-09-302-495-5	Sequence 5, Appli
	893	15	0.9	2193	4	US-10-079-616-5	Sequence 5, Appli
c	894	15	0.9	2226	1	US-08-299-849B-16	Sequence 16, Appl
c	895	15	0.9	2226	2	US-08-142-368A-16	Sequence 16, Appl
c	896	15	0.9	2226	3	US-08-967-727-16	Sequence 16, Appl
c	897	15	0.9	2226	3	US-08-037-230D-16	Sequence 16, Appl
c	898	15	0.9	2226	4	US-09-583-850-16	Sequence 16, Appl
c	899	15	0.9	2226	4	US-09-579-197-16	Sequence 16, Appl
c	900	15	0.9	2226	4	US-09-404-026-16	Sequence 16, Appl
c	901	15	0.9	2226	4	US-09-312-464-16	Sequence 16, Appl
c	902	15	0.9	2230	4	US-09-620-312D-282	Sequence 282, App
c	903	15	0.9	2270	2	US-08-852-807-16	Sequence 16, Appl
c	904	15	0.9	2274	4	US-09-799-451-149	Sequence 149, App
	905	15	0.9	2291	2	US-08-725-736D-1	Sequence 1, Appli
	906	15	0.9	2291	3	US-09-162-368B-1	Sequence 1, Appli
	907	15	0.9	2291	3	US-09-161-877B-1	Sequence 1, Appli
c	908	15	0.9	2305	1	US-08-299-849B-17	Sequence 17, Appl
c	909	15	0.9	2305	2	US-08-142-368A-17	Sequence 17, Appl
c	910	15	0.9	2305	3	US-08-967-727-17	Sequence 17, Appl
c	911	15	0.9	2305	3	US-08-037-230D-17	Sequence 17, Appl
c	912	15	0.9	2305	4	US-09-583-850-17	Sequence 17, Appl
c	913	15	0.9	2305	4	US-09-579-197-17	Sequence 17, Appl
c	914	15	0.9	2305	4	US-09-404-026-17	Sequence 17, Appl
	915	15	0.9	2308	4	US-09-835-654-4	Sequence 4, Appli
	916	15	0.9	2318	4	US-09-851-062-3	Sequence 3, Appli
	917	15	0.9	2346	3	US-09-193-503B-4	Sequence 4, Appli
	918	15	0.9	2346	3	US-09-193-503B-5	Sequence 5, Appli
	919	15	0.9	2346	3	US-09-193-503B-8	Sequence 8, Appli
	920	15	0.9	2346	4	US-09-415-839-4	Sequence 4, Appli
	921	15	0.9	2346	4	US-09-415-839-5	Sequence 5, Appli
	922	15	0.9	2346	4	US-09-415-839-8	Sequence 8, Appli
	923	15	0.9	2362	1	US-08-265-087-1	Sequence 1, Appli
	924	15	0.9	2362	1	US-08-621-493-1	Sequence 1, Appli
	925	15	0.9	2362	2	US-08-965-688-1	Sequence 1, Appli
	926	15	0.9	2362	3	US-09-260-173-1	Sequence 1, Appli
	927	15	0.9	2362	4	US-09-924-703-3	Sequence 3, Appli
	928	15	0.9	2395	3	US-08-985-335-6	Sequence 6, Appli
	929	15	0.9	2395	3	US-09-410-372-6	Sequence 6, Appli
	930	15	0.9	2422	3	US-08-952-365-7	Sequence 7, Appli
c	931	15	0.9	2442	4	US-09-131-237C-1	Sequence 1, Appli
c	932	15	0.9	2482	4	US-09-870-521-6	Sequence 6, Appli
	933	15	0.9	2524	4	US-08-961-527-242	Sequence 242, App
c	934	15	0.9	2571	4	US-09-598-401C-93	Sequence 93, Appl
	935	15	0.9	2597	4	US-09-835-654-1	Sequence 1, Appli
	936	15	0.9	2645	1	US-08-480-547A-22	Sequence 22, Appl
	937	15	0.9	2645	1	US-08-250-847B-22	Sequence 22, Appl
	938	15	0.9	2645	2	US-08-463-949A-22	Sequence 22, Appl
	939	15	0.9	2645	3	US-08-464-410A-22	Sequence 22, Appl
	940	15	0.9	2645	5	PCT-US94-06066-22	Sequence 22, Appl
	941	15	0.9	2688	1	US-08-088-633-3	Sequence 3, Appli
	942	15	0.9	2688	1	US-08-245-756-3	Sequence 3, Appli
	943	15	0.9	2688	1	US-08-441-750-3	Sequence 3, Appli
	944	15	0.9	2688	2	US-08-441-751-3	Sequence 3, Appli
	945	15	0.9	2688	5	PCT-US92-02521-3	Sequence 3, Appli
	946	15	0.9	2709	4	US-09-107-532A-183	Sequence 183, App
	947	15	0.9	2733	4	US-09-614-221A-372	Sequence 372, App
	948	15	0.9	2734	4	US-09-620-312D-533	Sequence 533, App
	949	15	0.9	2754	3	US-09-429-322-3	Sequence 3, Appli
	950	15	0.9	2802	4	US-09-976-594-924	Sequence 924, App
c	951	15	0.9	2896	2	US-08-709-923-1	Sequence 1, Appli
	952	15	0.9	2903	3	US-08-928-941D-2	Sequence 2, Appli
	953	15	0.9	2903	3	US-08-928-941D-3	Sequence 3, Appli
	954	15	0.9	2903	3	US-09-280-590A-2	Sequence 2, Appli
	955	15	0.9	2903	3	US-09-280-590A-3	Sequence 3, Appli
	956	15	0.9	2903	4	US-09-892-398-2	Sequence 2, Appli
	957	15	0.9	2903	4	US-09-892-398-3	Sequence 3, Appli
	958	15	0.9	2909	3	US-08-104-158-1	Sequence 1, Appli
	959	15	0.9	2909	4	US-09-609-040-1	Sequence 1, Appli
	960	15	0.9	2979	4	US-09-437-277-4	Sequence 4, Appli
	961	15	0.9	2992	1	US-07-718-575-1	Sequence 1, Appli
	962	15	0.9	2992	1	US-08-481-206-1	Sequence 1, Appli
	963	15	0.9	2992	2	US-08-486-269A-1	Sequence 1, Appli
c	964	15	0.9	2998	4	US-09-710-279-3894	Sequence 3894, Ap
c	965	15	0.9	3006	4	US-09-248-796A-3676	Sequence 3676, Ap
c	966	15	0.9	3055	4	US-08-956-171E-297	Sequence 297, App
c	967	15	0.9	3055	4	US-08-781-986A-297	Sequence 297, App
c	968	15	0.9	3075	4	US-09-023-655-1369	Sequence 1369, Ap
c	969	15	0.9	3079	4	US-09-053-374A-6	Sequence 6, Appli
c	970	15	0.9	3083	4	US-09-155-246-1	Sequence 1, Appli
	971	15	0.9	3118	4	US-09-710-279-3798	Sequence 3798, Ap
	972	15	0.9	3128	3	US-08-716-449-1	Sequence 1, Appli
c	973	15	0.9	3141	4	US-09-252-991A-13713	Sequence 13713, A
c	974	15	0.9	3150	3	US-08-673-814-5	Sequence 5, Appli
c	975	15	0.9	3150	3	US-09-115-824-5	Sequence 5, Appli
	976	15	0.9	3158	4	US-09-710-279-4054	Sequence 4054, Ap

977	15	0.9	3177	4	US-09-248-796A-5784	Sequence 5784, Ap
c 978	15	0.9	3182	4	US-09-155-885A-305	Sequence 305, App
c 979	15	0.9	3188	4	US-09-710-279-3837	Sequence 3837, Ap
c 980	15	0.9	3188	4	US-09-155-885A-293	Sequence 293, App
c 981	15	0.9	3200	4	US-09-155-885A-280	Sequence 280, App
982	15	0.9	3211	2	US-08-574-959A-8	Sequence 8, Appli
983	15	0.9	3211	3	US-09-357-014-8	Sequence 8, Appli
984	15	0.9	3212	3	US-08-673-814-1	Sequence 1, Appli
985	15	0.9	3212	3	US-09-115-824-1	Sequence 1, Appli
c 986	15	0.9	3212	4	US-09-155-885A-298	Sequence 298, App
c 987	15	0.9	3213	4	US-09-155-885A-288	Sequence 288, App
c 988	15	0.9	3213	4	US-09-155-885A-289	Sequence 289, App
c 989	15	0.9	3214	4	US-09-155-885A-294	Sequence 294, App
c 990	15	0.9	3215	4	US-09-719-528A-1	Sequence 1, Appli
c 991	15	0.9	3215	4	US-09-155-885A-290	Sequence 290, App
c 992	15	0.9	3215	4	US-09-155-885A-291	Sequence 291, App
c 993	15	0.9	3215	4	US-09-155-885A-292	Sequence 292, App
c 994	15	0.9	3215	4	US-09-155-885A-295	Sequence 295, App
c 995	15	0.9	3215	4	US-09-155-885A-296	Sequence 296, App
c 996	15	0.9	3215	4	US-09-155-885A-297	Sequence 297, App
c 997	15	0.9	3215	4	US-10-209-264-1	Sequence 1, Appli
c 998	15	0.9	3220	2	US-08-225-488-1	Sequence 1, Appli
c 999	15	0.9	3220	6	5196194-11	Patent No. 5196194
c1000	15	0.9	3220	6	5196194-15	Patent No. 5196194

ALIGNMENTS

```
RESULT 1
US-09-248-796A-11388
; Sequence 11388, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 11388
;   LENGTH: 198
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-11388

  Query Match             1.2%;  Score 19;  DB 4;  Length 198;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1617 GGAGCTTGATAAAAGTGGG 1635
              |||||||||||||||||||
Db          2 GGAGCTTGATAAAAGTGGG 20


RESULT 2
US-08-956-171E-107
; Sequence 107, Application US/08956171E
; Patent No. 6593114
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/956,171E
;             FILING DATE: 20-Oct-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;    INFORMATION FOR SEQ ID NO: 107:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2488 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-08-956-171E-107

  Query Match             1.2%;  Score 19;  DB 4;  Length 2488;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        923 AATATCAATCAAAATATTC 941
              |||||||||||||||||||
Db       1354 AATATCAATCAAAATATTC 1372


RESULT 3
US-08-781-986A-107
; Sequence 107, Application US/08781986A
; Patent No. 6737248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2488 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-107

  Query Match             1.2%;  Score 19;  DB 4;  Length 2488;
  Best Local Similarity   100.0%;  Pred. No. 8.2;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        923 AATATCAATCAAAATATTC 941
              |||||||||||||||||||
Db       1354 AATATCAATCAAAATATTC 1372


RESULT 4
US-09-513-999C-16375
; Sequence 16375, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 16375
;   LENGTH: 125
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-16375

  Query Match             1.1%;  Score 18;  DB 4;  Length 125;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1111 GATAGCAAGAGGATGTTA 1128
              ||||||||||||||||||
Db         49 GATAGCAAGAGGATGTTA 66


RESULT 5
US-09-513-999C-23083
; Sequence 23083, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 23083
;   LENGTH: 153
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-513-999C-23083

  Query Match             1.1%;  Score 18;  DB 4;  Length 153;
  Best Local Similarity   100.0%;  Pred. No. 25;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1161 TGTTTTTAATCCTCTGAC 1178
              ||||||||||||||||||
Db        107 TGTTTTTAATCCTCTGAC 124


RESULT 6
US-09-134-001C-396/c
; Sequence 396, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 396
;   LENGTH: 186
;   TYPE: DNA
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-396

  Query Match             1.1%;  Score 18;  DB 3;  Length 186;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        954 AAATATTATTAACATTGA 971
              ||||||||||||||||||
Db         37 AAATATTATTAACATTGA 20


RESULT 7
US-09-389-681-371
; Sequence 371, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
;  APPLICANT: Yuqui, Jiang
;  APPLICANT: Dillon, Davin C.
;  APPLICANT: Mitcham, Jennifer L.
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
;  TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.470C3
;  CURRENT APPLICATION NUMBER: US/09/389,681A
;  CURRENT FILING DATE: 1999-09-02
;  NUMBER OF SEQ ID NOS: 463
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 371
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-389-681-371

  Query Match             1.1%;  Score 18;  DB 4;  Length 241;
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Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115
```

RESULT 8
US-09-620-405B-371
; Sequence 371, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-620-405B-371

Query Match 1.1%; Score 18; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115
```

RESULT 9
US-09-433-826B-371
; Sequence 371, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqui
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-433-826B-371

Query Match 1.1%; Score 18; DB 4; Length 241;

Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115
```

RESULT 10
US-09-604-287A-371
; Sequence 371, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-604-287A-371

Query Match 1.1%; Score 18; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115
```

RESULT 11
US-09-834-759-371
; Sequence 371, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(241)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-759-371

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  Query Match             1.1%;  Score 18;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115


RESULT 12
US-09-590-751A-371
; Sequence 371, Application US/09590751A
; Patent No. 6756477
; GENERAL INFORMATION:
;  APPLICANT:  Yuqui, Jiang
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION:  COMPOSITIONS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF BREAST CANCER
;  FILE REFERENCE:  210121.470C6
;  CURRENT APPLICATION NUMBER: US/09/590,751A
;  CURRENT FILING DATE:  2000-06-08
;  NUMBER OF SEQ ID NOS:  479
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 371
;   LENGTH: 241
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(241)
;   OTHER INFORMATION: n = A,T,C or G
US-09-590-751A-371

  Query Match             1.1%;  Score 18;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        648 TTATTTGAAGTGGCTTGA 665
              ||||||||||||||||||
Db         98 TTATTTGAAGTGGCTTGA 115


RESULT 13
US-09-643-597-325
; Sequence 325, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE:  2000-08-21
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; Sequence 325, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C6
;  CURRENT APPLICATION NUMBER: US/09/480,884A
;  CURRENT FILING DATE:  2001-08-27
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RESULT 15
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; Sequence 325, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
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;  CURRENT APPLICATION NUMBER: US/09/542,615A
;  CURRENT FILING DATE:  2000-04-14
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;   ORGANISM: Homo sapien
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c	195	17	1.0	590	16	US-10-424-599-140605	Sequence 140605,
c	196	17	1.0	593	10	US-09-822-846-214	Sequence 214, App
	197	17	1.0	603	13	US-10-027-632-44575	Sequence 44575, A
	198	17	1.0	603	15	US-10-027-632-44575	Sequence 44575, A
	199	17	1.0	612	16	US-10-424-599-47383	Sequence 47383, A
c	200	17	1.0	622	13	US-10-027-632-90780	Sequence 90780, A
c	201	17	1.0	622	13	US-10-027-632-90781	Sequence 90781, A
c	202	17	1.0	622	15	US-10-027-632-90780	Sequence 90780, A
c	203	17	1.0	622	15	US-10-027-632-90781	Sequence 90781, A
	204	17	1.0	625	16	US-10-424-599-128229	Sequence 128229,
c	205	17	1.0	628	13	US-10-027-632-243608	Sequence 243608,
c	206	17	1.0	628	15	US-10-027-632-243608	Sequence 243608,
	207	17	1.0	643	17	US-10-767-701-5903	Sequence 5903, Ap
c	208	17	1.0	645	13	US-10-027-632-240102	Sequence 240102,
c	209	17	1.0	645	15	US-10-027-632-240102	Sequence 240102,
	210	17	1.0	649	16	US-10-424-599-135113	Sequence 135113,
	211	17	1.0	656	13	US-10-027-632-66140	Sequence 66140, A
	212	17	1.0	656	15	US-10-027-632-66140	Sequence 66140, A
c	213	17	1.0	663	9	US-09-841-132-409	Sequence 409, App
c	214	17	1.0	663	13	US-10-027-632-88922	Sequence 88922, A
	215	17	1.0	663	13	US-10-027-632-320486	Sequence 320486,
c	216	17	1.0	663	15	US-10-027-632-88922	Sequence 88922, A
	217	17	1.0	663	15	US-10-027-632-320486	Sequence 320486,
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c	219	17	1.0	670	13	US-10-027-632-109991	Sequence 109991,
c	220	17	1.0	670	15	US-10-027-632-109990	Sequence 109990,
c	221	17	1.0	670	15	US-10-027-632-109991	Sequence 109991,
	222	17	1.0	704	13	US-10-027-632-70647	Sequence 70647, A
	223	17	1.0	704	15	US-10-027-632-70647	Sequence 70647, A
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	225	17	1.0	713	18	US-10-425-115-158251	Sequence 158251,
	226	17	1.0	727	13	US-10-027-632-117525	Sequence 117525,
	227	17	1.0	727	15	US-10-027-632-117525	Sequence 117525,
c	228	17	1.0	729	17	US-10-767-701-26740	Sequence 26740, A
	229	17	1.0	736	13	US-10-027-632-147995	Sequence 147995,
	230	17	1.0	736	13	US-10-027-632-147996	Sequence 147996,
	231	17	1.0	736	15	US-10-027-632-147995	Sequence 147995,

	232	17	1.0	736	15	US-10-027-632-147996 Sequence 147996,
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c	234	17	1.0	742	15	US-10-027-632-27520 Sequence 27520, A
	235	17	1.0	747	16	US-10-424-599-33187 Sequence 33187, A
	236	17	1.0	753	13	US-10-027-632-167628 Sequence 167628,
	237	17	1.0	753	15	US-10-027-632-167628 Sequence 167628,
c	238	17	1.0	754	16	US-10-305-720-43 Sequence 43, Appl
c	239	17	1.0	760	10	US-09-873-367C-963 Sequence 963, App
c	240	17	1.0	760	11	US-09-968-007A-513 Sequence 513, App
c	241	17	1.0	764	18	US-10-425-115-89839 Sequence 89839, A
	242	17	1.0	784	16	US-10-424-599-106597 Sequence 106597,
c	243	17	1.0	793	9	US-09-925-302-349 Sequence 349, App
c	244	17	1.0	793	10	US-09-925-302-349 Sequence 349, App
c	245	17	1.0	803	15	US-10-172-118-853 Sequence 853, App
c	246	17	1.0	803	15	US-10-295-027-964 Sequence 964, App
c	247	17	1.0	803	16	US-10-058-270A-99 Sequence 99, Appl
c	248	17	1.0	803	16	US-10-240-425-1574 Sequence 1574, Ap
c	249	17	1.0	803	16	US-10-342-887-853 Sequence 853, App
	250	17	1.0	807	13	US-10-078-929-7 Sequence 7, Appli
	251	17	1.0	809	17	US-10-437-963-65162 Sequence 65162, A
c	252	17	1.0	810	16	US-10-282-122A-7140 Sequence 7140, Ap
	253	17	1.0	819	9	US-09-770-445-736 Sequence 736, App
c	254	17	1.0	823	16	US-10-424-599-59287 Sequence 59287, A
c	255	17	1.0	834	15	US-10-369-493-34753 Sequence 34753, A
	256	17	1.0	846	14	US-10-144-929-62 Sequence 62, Appl
	257	17	1.0	846	16	US-10-144-929-62 Sequence 62, Appl
c	258	17	1.0	883	13	US-10-027-632-120497 Sequence 120497,
c	259	17	1.0	883	13	US-10-027-632-120498 Sequence 120498,
c	260	17	1.0	883	15	US-10-027-632-120497 Sequence 120497,
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	262	17	1.0	980	16	US-10-260-238-5103 Sequence 5103, Ap
	263	17	1.0	1026	13	US-10-078-929-9 Sequence 9, Appli
c	264	17	1.0	1043	13	US-10-027-632-252199 Sequence 252199,
c	265	17	1.0	1043	15	US-10-027-632-252199 Sequence 252199,
	266	17	1.0	1083	9	US-09-938-842A-2223 Sequence 2223, Ap
	267	17	1.0	1083	11	US-09-938-842A-2223 Sequence 2223, Ap
	268	17	1.0	1098	13	US-10-027-632-308014 Sequence 308014,
	269	17	1.0	1098	15	US-10-027-632-308014 Sequence 308014,
	270	17	1.0	1272	16	US-10-425-114-35730 Sequence 35730, A
c	271	17	1.0	1300	13	US-10-027-632-90782 Sequence 90782, A
c	272	17	1.0	1300	15	US-10-027-632-90782 Sequence 90782, A
	273	17	1.0	1311	18	US-10-425-115-181250 Sequence 181250,
c	274	17	1.0	1388	9	US-09-954-456-1149 Sequence 1149, Ap
c	275	17	1.0	1388	9	US-09-954-456-1814 Sequence 1814, Ap
c	276	17	1.0	1389	15	US-10-172-118-673 Sequence 673, App
c	277	17	1.0	1389	16	US-10-342-887-673 Sequence 673, App
c	278	17	1.0	1413	18	US-10-739-930-1662 Sequence 1662, Ap
c	279	17	1.0	1462	17	US-10-437-963-31823 Sequence 31823, A
	280	17	1.0	1500	16	US-10-424-599-75802 Sequence 75802, A
	281	17	1.0	1521	16	US-10-424-599-59503 Sequence 59503, A
c	282	17	1.0	1551	15	US-10-369-493-45615 Sequence 45615, A
c	283	17	1.0	1551	17	US-10-477-369-62 Sequence 62, Appl
c	284	17	1.0	1551	18	US-10-793-639-531 Sequence 531, App
	285	17	1.0	1584	18	US-10-425-115-80977 Sequence 80977, A
	286	17	1.0	1606	16	US-10-425-114-8184 Sequence 8184, Ap
c	287	17	1.0	1683	15	US-10-115-831-22 Sequence 22, Appl
c	288	17	1.0	1733	18	US-10-425-115-15006 Sequence 15006, A
c	289	17	1.0	1750	15	US-10-071-179-28 Sequence 28, Appl
c	290	17	1.0	1750	15	US-10-126-704-28 Sequence 28, Appl
	291	17	1.0	1760	16	US-10-424-599-16008 Sequence 16008, A
	292	17	1.0	1813	16	US-10-424-599-75941 Sequence 75941, A
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	294	17	1.0	1927	16	US-10-425-114-35689 Sequence 35689, A
	295	17	1.0	1934	15	US-10-369-493-44979 Sequence 44979, A
	296	17	1.0	1959	18	US-10-425-115-158511 Sequence 158511,
c	297	17	1.0	1989	15	US-10-369-493-43817 Sequence 43817, A
	298	17	1.0	1998	18	US-10-425-115-19473 Sequence 19473, A
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	300	17	1.0	2000	9	US-09-938-842A-4622 Sequence 4622, Ap
c	301	17	1.0	2000	11	US-09-938-842A-4002 Sequence 4002, Ap
	302	17	1.0	2000	11	US-09-938-842A-4622 Sequence 4622, Ap
c	303	17	1.0	2006	16	US-10-220-120-206 Sequence 206, App
c	304	17	1.0	2018	9	US-09-764-869-1568 Sequence 1568, Ap
c	305	17	1.0	2018	14	US-10-091-504-1568 Sequence 1568, Ap
c	306	17	1.0	2018	16	US-10-227-577-1568 Sequence 1568, Ap
	307	17	1.0	2026	18	US-10-425-115-174840 Sequence 174840,
	308	17	1.0	2063	15	US-10-104-047-455 Sequence 455, App
c	309	17	1.0	2154	9	US-09-801-368-375 Sequence 375, App
	310	17	1.0	2194	16	US-10-424-599-106594 Sequence 106594,
c	311	17	1.0	2200	8	US-08-899-112-9 Sequence 9, Appli
c	312	17	1.0	2200	15	US-10-298-992-3 Sequence 3, Appli
c	313	17	1.0	2200	15	US-10-285-019-9 Sequence 9, Appli
c	314	17	1.0	2217	15	US-10-369-493-25507 Sequence 25507, A
	315	17	1.0	2235	16	US-10-282-122A-41550 Sequence 41550, A
	316	17	1.0	2301	18	US-10-425-115-4212 Sequence 4212, Ap
	317	17	1.0	2310	16	US-10-282-122A-18020 Sequence 18020, A
c	318	17	1.0	2324	16	US-10-424-599-37749 Sequence 37749, A
	319	17	1.0	2366	16	US-10-424-599-106595 Sequence 106595,
	320	17	1.0	2380	17	US-10-437-963-16586 Sequence 16586, A
c	321	17	1.0	2427	13	US-10-027-632-111380 Sequence 111380,
c	322	17	1.0	2427	15	US-10-027-632-111380 Sequence 111380,
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	324	17	1.0	2548	15	US-10-177-573-4 Sequence 4, Appli
c	325	17	1.0	2553	17	US-10-437-963-11782 Sequence 11782, A
	326	17	1.0	2601	16	US-10-282-122A-24723 Sequence 24723, A
	327	17	1.0	2674	10	US-09-814-353-19921 Sequence 19921, A
	328	17	1.0	2732	17	US-10-377-139-17 Sequence 17, Appl
	329	17	1.0	2773	17	US-10-437-963-34050 Sequence 34050, A
	330	17	1.0	2781	16	US-10-108-260A-785 Sequence 785, App
c	331	17	1.0	2799	9	US-09-764-870-220 Sequence 220, App
c	332	17	1.0	2799	14	US-10-125-540-220 Sequence 220, App
	333	17	1.0	2822	16	US-10-108-260A-1263 Sequence 1263, Ap
c	334	17	1.0	2975	16	US-10-398-221-2005 Sequence 2005, Ap
	335	17	1.0	3044	9	US-09-764-870-98 Sequence 98, Appl
	336	17	1.0	3044	14	US-10-125-540-98 Sequence 98, Appl
c	337	17	1.0	3132	16	US-10-108-260A-679 Sequence 679, App
c	338	17	1.0	3140	15	US-10-369-493-26760 Sequence 26760, A
c	339	17	1.0	3145	14	US-10-116-802-319 Sequence 319, App
	340	17	1.0	3146	18	US-10-425-115-3092 Sequence 3092, Ap
	341	17	1.0	3150	17	US-10-437-963-7292 Sequence 7292, Ap
	342	17	1.0	3433	16	US-10-424-599-128232 Sequence 128232,
	343	17	1.0	3524	17	US-10-437-963-7622 Sequence 7622, Ap
c	344	17	1.0	3546	17	US-10-437-963-54272 Sequence 54272, A
c	345	17	1.0	3634	17	US-10-322-281-156 Sequence 156, App
	346	17	1.0	3715	15	US-10-094-749-1066 Sequence 1066, Ap
c	347	17	1.0	3846	16	US-10-276-774-418 Sequence 418, App
c	348	17	1.0	4071	16	US-10-398-221-3646 Sequence 3646, Ap
	349	17	1.0	4140	15	US-10-161-927-23 Sequence 23, Appl
c	350	17	1.0	4149	15	US-10-010-160-17 Sequence 17, Appl
c	351	17	1.0	4214	13	US-10-194-163-293 Sequence 293, App
c	352	17	1.0	4226	15	US-10-037-270-480 Sequence 480, App
c	353	17	1.0	4226	15	US-10-117-722-480 Sequence 480, App
	354	17	1.0	4277	18	US-10-425-115-26494 Sequence 26494, A
c	355	17	1.0	4674	16	US-10-221-625-202 Sequence 202, App
	356	17	1.0	5343	16	US-10-062-674-1951 Sequence 1951, Ap
c	357	17	1.0	5659	13	US-10-002-600-80 Sequence 80, Appl
c	358	17	1.0	5763	13	US-10-002-600-79 Sequence 79, Appl
c	359	17	1.0	6002	15	US-10-071-179-4 Sequence 4, Appli
c	360	17	1.0	6002	15	US-10-126-704-4 Sequence 4, Appli
	361	17	1.0	7786	9	US-09-790-988-2 Sequence 2, Appli
	362	17	1.0	11169	17	US-10-433-793-125 Sequence 125, App
	363	17	1.0	11622	15	US-10-311-455-648 Sequence 648, App
c	364	17	1.0	19734	15	US-10-311-455-1905 Sequence 1905, Ap
c	365	17	1.0	22744	11	US-09-997-722-181 Sequence 181, App
c	366	17	1.0	23745	13	US-10-087-192-1429 Sequence 1429, Ap
	367	17	1.0	23965	17	US-10-367-094-139 Sequence 139, App
c	368	17	1.0	24800	11	US-09-997-722-187 Sequence 187, App
c	369	17	1.0	25231	10	US-09-764-891-5800 Sequence 5800, Ap
c	370	17	1.0	28001	15	US-10-173-817-11 Sequence 11, Appl
c	371	17	1.0	28001	15	US-10-173-817-12 Sequence 12, Appl
c	372	17	1.0	28001	16	US-10-643-432-11 Sequence 11, Appl
c	373	17	1.0	28001	16	US-10-643-432-12 Sequence 12, Appl
	374	17	1.0	28454	13	US-10-087-192-316 Sequence 316, App
c	375	17	1.0	29521	15	US-10-074-024-471 Sequence 471, App
c	376	17	1.0	29543	15	US-10-074-024-470 Sequence 470, App
	377	17	1.0	30821	13	US-10-087-192-1276 Sequence 1276, Ap

c 378	17	1.0	32038	9	US-09-764-878-292	Sequence 292, App
c 379	17	1.0	32038	14	US-10-079-854-292	Sequence 292, App
380	17	1.0	32844	11	US-09-984-429-498	Sequence 498, App
c 381	17	1.0	38753	17	US-10-741-601-5767	Sequence 5767, Ap
382	17	1.0	47243	13	US-10-087-192-1264	Sequence 1264, Ap
c 383	17	1.0	50000	14	US-10-152-724A-20	Sequence 20, Appl
384	17	1.0	52302	11	US-09-997-722-4	Sequence 4, Appli
385	17	1.0	55001	15	US-10-160-497-4	Sequence 4, Appli
386	17	1.0	55001	15	US-10-348-750-4	Sequence 4, Appli
c 387	17	1.0	63155	15	US-10-292-798-449	Sequence 449, App
c 388	17	1.0	65359	9	US-09-804-472-3	Sequence 3, Appli
c 389	17	1.0	67076	13	US-10-087-192-1753	Sequence 1753, Ap
c 390	17	1.0	71292	13	US-10-087-192-1942	Sequence 1942, Ap
c 391	17	1.0	72678	17	US-10-322-281-214	Sequence 214, App
392	17	1.0	75252	13	US-10-087-192-904	Sequence 904, App
c 393	17	1.0	86001	17	US-10-317-500-4	Sequence 4, Appli
c 394	17	1.0	96597	16	US-10-052-482-103	Sequence 103, App
c 395	17	1.0	106344	10	US-09-910-185-10	Sequence 10, Appl
c 396	17	1.0	107280	17	US-10-322-281-155	Sequence 155, App
c 397	17	1.0	128668	13	US-10-087-192-340	Sequence 340, App
c 398	17	1.0	133300	18	US-10-331-053-70	Sequence 70, Appl
c 399	17	1.0	139257	10	US-09-920-671-11	Sequence 11, Appl
c 400	17	1.0	144723	13	US-10-087-192-1576	Sequence 1576, Ap
401	17	1.0	158091	16	US-10-235-192A-38	Sequence 38, Appl
c 402	17	1.0	162450	15	US-10-071-179-1	Sequence 1, Appli
c 403	17	1.0	162450	15	US-10-126-704-1	Sequence 1, Appli
404	17	1.0	163382	17	US-10-367-094-179	Sequence 179, App
c 405	17	1.0	163382	17	US-10-367-094-179	Sequence 179, App
406	17	1.0	174566	14	US-10-020-141-1	Sequence 1, Appli
407	17	1.0	174566	16	US-10-235-192A-37	Sequence 37, Appl
408	17	1.0	197997	9	US-09-822-246-3	Sequence 3, Appli
c 409	17	1.0	208700	17	US-10-388-838-4	Sequence 4, Appli
410	17	1.0	220224	13	US-10-087-192-1282	Sequence 1282, Ap
c 411	17	1.0	275449	13	US-10-087-192-520	Sequence 520, App
412	17	1.0	295096	13	US-10-087-192-331	Sequence 331, App
c 413	17	1.0	317876	17	US-10-741-601-5629	Sequence 5629, Ap
414	17	1.0	335913	10	US-09-754-853A-2	Sequence 2, Appli
415	17	1.0	335913	10	US-09-754-853A-3	Sequence 3, Appli
416	17	1.0	374849	13	US-10-087-192-1627	Sequence 1627, Ap
417	17	1.0	397658	9	US-09-813-320-3	Sequence 3, Appli
c 418	17	1.0	397658	9	US-09-813-320-3	Sequence 3, Appli
c 419	17	1.0	483728	18	US-10-699-156-2	Sequence 2, Appli
c 420	17	1.0	518360	17	US-10-367-094-125	Sequence 125, App
421	17	1.0	684187	17	US-10-367-094-71	Sequence 71, Appl
c 422	17	1.0	1163020	16	US-10-398-221-10	Sequence 10, Appl
c 423	17	1.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 424	17	1.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
c 425	17	1.0	1503841	9	US-09-946-807-1	Sequence 1, Appli
c 426	17	1.0	1691139	14	US-10-067-514-1	Sequence 1, Appli
c 427	17	1.0	1691139	16	US-10-419-723-1	Sequence 1, Appli
428	17	1.0	2140405	13	US-10-027-632-76212	Sequence 76212, A
429	17	1.0	2140405	15	US-10-027-632-76212	Sequence 76212, A
c 430	17	1.0	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
c 431	17	1.0	3673778	15	US-10-312-841-1	Sequence 1, Appli
432	17	1.0	3673778	15	US-10-312-841-2	Sequence 2, Appli
c 433	16	1.0	25	10	US-09-771-933-27	Sequence 27, Appl
434	16	1.0	25	10	US-09-771-933-34	Sequence 34, Appl
c 435	16	1.0	25	10	US-09-771-933-35	Sequence 35, Appl
436	16	1.0	25	10	US-09-771-933-205	Sequence 205, App
437	16	1.0	25	15	US-10-098-263B-64897	Sequence 64897, A
438	16	1.0	25	15	US-10-098-263B-111372	Sequence 111372,
439	16	1.0	60	10	US-09-908-975-5324	Sequence 5324, Ap
440	16	1.0	65	10	US-09-908-975-1511	Sequence 1511, Ap
c 441	16	1.0	88	15	US-10-029-386-14801	Sequence 14801, A
442	16	1.0	112	10	US-09-764-891-10079	Sequence 10079, A
443	16	1.0	112	10	US-09-764-891-10080	Sequence 10080, A
444	16	1.0	112	15	US-10-205-428-989	Sequence 989, App
445	16	1.0	112	15	US-10-205-428-990	Sequence 990, App
446	16	1.0	116	9	US-09-864-761-27222	Sequence 27222, A
447	16	1.0	116	16	US-10-424-599-36191	Sequence 36191, A
448	16	1.0	122	16	US-10-424-599-92078	Sequence 92078, A
449	16	1.0	125	17	US-10-437-963-96352	Sequence 96352, A
c 450	16	1.0	129	9	US-09-864-761-28284	Sequence 28284, A
451	16	1.0	129	16	US-10-242-535A-46002	Sequence 46002, A
452	16	1.0	129	16	US-10-085-783A-46002	Sequence 46002, A
c 453	16	1.0	140	9	US-09-736-457-1392	Sequence 1392, Ap
c 454	16	1.0	140	9	US-09-902-941-1392	Sequence 1392, Ap
c 455	16	1.0	140	9	US-09-849-626-1392	Sequence 1392, Ap
c 456	16	1.0	140	14	US-10-017-754-1392	Sequence 1392, Ap
c 457	16	1.0	140	15	US-10-113-872-1392	Sequence 1392, Ap
c 458	16	1.0	140	15	US-10-283-017-1392	Sequence 1392, Ap
459	16	1.0	144	9	US-09-864-761-28253	Sequence 28253, A
c 460	16	1.0	156	9	US-09-864-761-32118	Sequence 32118, A
461	16	1.0	185	14	US-10-198-846-9760	Sequence 9760, Ap
c 462	16	1.0	185	16	US-10-424-599-100675	Sequence 100675,
463	16	1.0	189	14	US-10-010-731-18	Sequence 18, Appl
c 464	16	1.0	198	15	US-10-029-386-26040	Sequence 26040, A
465	16	1.0	199	9	US-09-896-096A-8	Sequence 8, Appli
466	16	1.0	199	9	US-09-894-924-8	Sequence 8, Appli
467	16	1.0	199	16	US-10-456-819-8	Sequence 8, Appli
468	16	1.0	199	17	US-10-688-132-8	Sequence 8, Appli
469	16	1.0	200	14	US-10-010-731-5	Sequence 5, Appli
470	16	1.0	201	17	US-10-741-601-23146	Sequence 23146, A
471	16	1.0	201	17	US-10-741-601-23778	Sequence 23778, A
c 472	16	1.0	204	15	US-10-029-386-15612	Sequence 15612, A
473	16	1.0	205	9	US-09-960-352-12271	Sequence 12271, A
474	16	1.0	206	9	US-09-864-761-30400	Sequence 30400, A
c 475	16	1.0	210	17	US-10-437-963-42187	Sequence 42187, A
c 476	16	1.0	212	9	US-09-796-692-6002	Sequence 6002, Ap
c 477	16	1.0	212	14	US-10-040-862-6002	Sequence 6002, Ap
c 478	16	1.0	212	16	US-10-057-475B-6002	Sequence 6002, Ap
c 479	16	1.0	212	16	US-10-154-884B-6002	Sequence 6002, Ap
c 480	16	1.0	212	17	US-10-764-324-6002	Sequence 6002, Ap
c 481	16	1.0	215	9	US-09-960-352-10302	Sequence 10302, A
c 482	16	1.0	220	15	US-10-029-386-21235	Sequence 21235, A
c 483	16	1.0	225	16	US-10-424-599-103228	Sequence 103228,
484	16	1.0	233	9	US-09-292-758-141	Sequence 141, App
485	16	1.0	237	10	US-09-814-353-14029	Sequence 14029, A
c 486	16	1.0	239	9	US-09-983-965-4783	Sequence 4783, Ap
487	16	1.0	242	18	US-10-425-115-144399	Sequence 144399,
c 488	16	1.0	245	16	US-10-242-535A-5776	Sequence 5776, Ap
c 489	16	1.0	245	16	US-10-085-783A-5776	Sequence 5776, Ap
c 490	16	1.0	249	13	US-10-016-634A-48	Sequence 48, Appl
c 491	16	1.0	249	17	US-10-437-963-8131	Sequence 8131, Ap
492	16	1.0	250	10	US-09-814-353-1170	Sequence 1170, Ap
493	16	1.0	250	10	US-09-814-353-7536	Sequence 7536, Ap
494	16	1.0	250	14	US-10-010-731-13	Sequence 13, Appl
c 495	16	1.0	252	13	US-10-071-751-46	Sequence 46, Appl
496	16	1.0	255	10	US-09-814-353-13922	Sequence 13922, A
c 497	16	1.0	255	10	US-09-930-213-465	Sequence 465, App
498	16	1.0	258	9	US-09-796-692-3471	Sequence 3471, Ap
499	16	1.0	258	14	US-10-040-862-3471	Sequence 3471, Ap
500	16	1.0	258	16	US-10-057-475B-3471	Sequence 3471, Ap
501	16	1.0	258	16	US-10-154-884B-3471	Sequence 3471, Ap
502	16	1.0	258	17	US-10-764-324-3471	Sequence 3471, Ap
503	16	1.0	259	9	US-09-294-093B-886	Sequence 886, App
c 504	16	1.0	261	9	US-09-983-965-5887	Sequence 5887, Ap
505	16	1.0	268	9	US-09-864-761-21966	Sequence 21966, A
506	16	1.0	269	16	US-10-424-599-94208	Sequence 94208, A
507	16	1.0	271	9	US-09-896-096A-5	Sequence 5, Appli
508	16	1.0	271	9	US-09-894-924-5	Sequence 5, Appli
509	16	1.0	271	16	US-10-456-819-5	Sequence 5, Appli
510	16	1.0	271	17	US-10-688-132-5	Sequence 5, Appli
511	16	1.0	273	9	US-09-764-877-2492	Sequence 2492, Ap
512	16	1.0	273	9	US-09-764-877-2493	Sequence 2493, Ap
513	16	1.0	273	16	US-10-242-515-2492	Sequence 2492, Ap
514	16	1.0	273	16	US-10-242-515-2493	Sequence 2493, Ap
515	16	1.0	277	9	US-09-896-096A-7	Sequence 7, Appli
516	16	1.0	277	9	US-09-894-924-7	Sequence 7, Appli
517	16	1.0	277	16	US-10-456-819-7	Sequence 7, Appli
518	16	1.0	277	17	US-10-688-132-7	Sequence 7, Appli
519	16	1.0	278	10	US-09-814-353-13920	Sequence 13920, A
520	16	1.0	283	9	US-09-896-096A-10	Sequence 10, Appl
521	16	1.0	283	9	US-09-894-924-10	Sequence 10, Appl
522	16	1.0	283	16	US-10-456-819-10	Sequence 10, Appl
523	16	1.0	283	17	US-10-688-132-10	Sequence 10, Appl

	524	16	1.0	290	10	US-09-814-353-1169	Sequence 1169, Ap
	525	16	1.0	290	10	US-09-814-353-7535	Sequence 7535, Ap
c	526	16	1.0	294	18	US-10-425-115-154141	Sequence 154141,
c	527	16	1.0	295	9	US-09-983-965-2678	Sequence 2678, Ap
	528	16	1.0	304	10	US-09-814-353-13921	Sequence 13921, A
	529	16	1.0	304	16	US-10-424-599-6284	Sequence 6284, Ap
	530	16	1.0	304	17	US-10-437-963-3627	Sequence 3627, Ap
	531	16	1.0	311	16	US-10-424-599-110099	Sequence 110099,
	532	16	1.0	312	10	US-09-814-353-1160	Sequence 1160, Ap
	533	16	1.0	312	10	US-09-814-353-7526	Sequence 7526, Ap
c	534	16	1.0	314	16	US-10-424-599-80113	Sequence 80113, A
	535	16	1.0	317	10	US-09-814-353-1210	Sequence 1210, Ap
	536	16	1.0	317	10	US-09-814-353-7576	Sequence 7576, Ap
c	537	16	1.0	318	18	US-10-425-115-58457	Sequence 58457, A
	538	16	1.0	322	10	US-09-814-353-1192	Sequence 1192, Ap
	539	16	1.0	322	10	US-09-814-353-7558	Sequence 7558, Ap
	540	16	1.0	324	10	US-09-814-353-1223	Sequence 1223, Ap
	541	16	1.0	324	10	US-09-814-353-7588	Sequence 7588, Ap
	542	16	1.0	325	10	US-09-814-353-13886	Sequence 13886, A
c	543	16	1.0	325	18	US-10-425-115-35203	Sequence 35203, A
	544	16	1.0	327	18	US-10-425-115-104450	Sequence 104450,
	545	16	1.0	328	10	US-09-814-353-3244	Sequence 3244, Ap
	546	16	1.0	328	10	US-09-814-353-9569	Sequence 9569, Ap
c	547	16	1.0	334	17	US-10-437-963-26833	Sequence 26833, A
c	548	16	1.0	340	10	US-09-803-719-1217	Sequence 1217, Ap
c	549	16	1.0	340	16	US-10-424-599-129176	Sequence 129176,
	550	16	1.0	343	13	US-10-087-192-1664	Sequence 1664, Ap
	551	16	1.0	344	10	US-09-814-353-1235	Sequence 1235, Ap
	552	16	1.0	344	10	US-09-814-353-7600	Sequence 7600, Ap
	553	16	1.0	347	10	US-09-814-353-1256	Sequence 1256, Ap
	554	16	1.0	347	10	US-09-814-353-7620	Sequence 7620, Ap
	555	16	1.0	348	16	US-10-242-535A-10328	Sequence 10328, A
	556	16	1.0	348	16	US-10-085-783A-10328	Sequence 10328, A
	557	16	1.0	350	10	US-09-814-353-1300	Sequence 1300, Ap
	558	16	1.0	350	10	US-09-814-353-7664	Sequence 7664, Ap
	559	16	1.0	351	18	US-10-425-115-137077	Sequence 137077,
	560	16	1.0	352	10	US-09-814-353-1205	Sequence 1205, Ap
	561	16	1.0	352	10	US-09-814-353-7571	Sequence 7571, Ap
c	562	16	1.0	352	16	US-10-242-535A-11300	Sequence 11300, A
c	563	16	1.0	352	16	US-10-085-783A-11300	Sequence 11300, A
	564	16	1.0	353	10	US-09-814-353-14005	Sequence 14005, A
	565	16	1.0	353	14	US-10-062-727-1031	Sequence 1031, Ap
	566	16	1.0	355	9	US-09-920-300A-1467	Sequence 1467, Ap
	567	16	1.0	355	10	US-09-814-353-1145	Sequence 1145, Ap
	568	16	1.0	355	10	US-09-814-353-7511	Sequence 7511, Ap
	569	16	1.0	355	13	US-10-033-528-1467	Sequence 1467, Ap
	570	16	1.0	355	15	US-10-099-926-1467	Sequence 1467, Ap
	571	16	1.0	356	10	US-09-814-353-1197	Sequence 1197, Ap
	572	16	1.0	356	10	US-09-814-353-7563	Sequence 7563, Ap
c	573	16	1.0	357	9	US-09-764-877-2816	Sequence 2816, Ap
	574	16	1.0	357	10	US-09-814-353-13984	Sequence 13984, A
c	575	16	1.0	357	16	US-10-242-515-2816	Sequence 2816, Ap
c	576	16	1.0	358	18	US-10-674-124A-9388	Sequence 9388, Ap
	577	16	1.0	360	10	US-09-814-353-1243	Sequence 1243, Ap
	578	16	1.0	360	10	US-09-814-353-7607	Sequence 7607, Ap
	579	16	1.0	361	11	US-09-732-627A-1953	Sequence 1953, Ap
c	580	16	1.0	361	16	US-10-621-901-1740	Sequence 1740, Ap
	581	16	1.0	362	10	US-09-814-353-13950	Sequence 13950, A
	582	16	1.0	363	10	US-09-814-353-1257	Sequence 1257, Ap
	583	16	1.0	363	10	US-09-814-353-7621	Sequence 7621, Ap
	584	16	1.0	363	16	US-10-242-535A-30632	Sequence 30632, A
	585	16	1.0	363	16	US-10-085-783A-30632	Sequence 30632, A
	586	16	1.0	363	18	US-10-425-115-139685	Sequence 139685,
c	587	16	1.0	364	10	US-09-918-995-18971	Sequence 18971, A
c	588	16	1.0	364	16	US-10-424-599-96615	Sequence 96615, A
	589	16	1.0	365	10	US-09-814-353-14006	Sequence 14006, A
	590	16	1.0	369	10	US-09-814-353-1302	Sequence 1302, Ap
	591	16	1.0	369	10	US-09-814-353-7666	Sequence 7666, Ap
	592	16	1.0	369	10	US-09-814-353-15953	Sequence 15953, A
	593	16	1.0	370	10	US-09-814-353-1304	Sequence 1304, Ap
	594	16	1.0	370	10	US-09-814-353-7668	Sequence 7668, Ap
c	595	16	1.0	370	18	US-10-425-115-149201	Sequence 149201,
	596	16	1.0	373	10	US-09-814-353-13973	Sequence 13973, A
c	597	16	1.0	375	9	US-09-777-564-152	Sequence 152, App
c	598	16	1.0	375	9	US-09-777-564-1488	Sequence 1488, Ap
c	599	16	1.0	375	14	US-10-015-219-152	Sequence 152, App
c	600	16	1.0	375	14	US-10-015-219-1488	Sequence 1488, Ap
	601	16	1.0	378	10	US-09-814-353-1270	Sequence 1270, Ap
	602	16	1.0	378	10	US-09-814-353-7634	Sequence 7634, Ap
	603	16	1.0	381	9	US-09-815-242-3231	Sequence 3231, Ap
	604	16	1.0	381	9	US-09-815-242-3315	Sequence 3315, Ap
	605	16	1.0	381	16	US-10-282-122A-5809	Sequence 5809, Ap
	606	16	1.0	381	16	US-10-282-122A-5887	Sequence 5887, Ap
	607	16	1.0	386	10	US-09-814-353-1200	Sequence 1200, Ap
	608	16	1.0	386	10	US-09-814-353-7566	Sequence 7566, Ap
	609	16	1.0	387	10	US-09-814-353-1164	Sequence 1164, Ap
	610	16	1.0	387	10	US-09-814-353-1299	Sequence 1299, Ap
	611	16	1.0	387	10	US-09-814-353-7530	Sequence 7530, Ap
	612	16	1.0	387	10	US-09-814-353-7663	Sequence 7663, Ap
c	613	16	1.0	390	9	US-09-960-352-6576	Sequence 6576, Ap
	614	16	1.0	390	10	US-09-814-353-1244	Sequence 1244, Ap
	615	16	1.0	390	10	US-09-814-353-7608	Sequence 7608, Ap
	616	16	1.0	391	16	US-10-424-599-28865	Sequence 28865, A
c	617	16	1.0	393	16	US-10-424-599-33260	Sequence 33260, A
	618	16	1.0	394	10	US-09-814-353-1127	Sequence 1127, Ap
	619	16	1.0	394	10	US-09-814-353-1251	Sequence 1251, Ap
	620	16	1.0	394	10	US-09-814-353-7493	Sequence 7493, Ap
	621	16	1.0	394	10	US-09-814-353-7615	Sequence 7615, Ap
	622	16	1.0	397	10	US-09-814-353-13896	Sequence 13896, A
	623	16	1.0	397	16	US-10-424-599-67060	Sequence 67060, A
c	624	16	1.0	399	10	US-09-918-995-7822	Sequence 7822, Ap
c	625	16	1.0	400	9	US-09-964-824A-19	Sequence 19, Appl
	626	16	1.0	400	10	US-09-814-353-13999	Sequence 13999, A
c	627	16	1.0	400	11	US-09-968-007A-41	Sequence 41, Appl
	628	16	1.0	401	10	US-09-814-353-1124	Sequence 1124, Ap
	629	16	1.0	401	10	US-09-814-353-7490	Sequence 7490, Ap
	630	16	1.0	401	16	US-10-424-599-136867	Sequence 136867,
	631	16	1.0	402	18	US-10-425-115-49171	Sequence 49171, A
	632	16	1.0	403	10	US-09-814-353-1185	Sequence 1185, Ap
	633	16	1.0	403	10	US-09-814-353-7551	Sequence 7551, Ap
	634	16	1.0	404	10	US-09-814-353-1275	Sequence 1275, Ap
	635	16	1.0	404	10	US-09-814-353-7639	Sequence 7639, Ap
	636	16	1.0	404	10	US-09-814-353-13911	Sequence 13911, A
c	637	16	1.0	404	16	US-10-424-599-1622	Sequence 1622, Ap
	638	16	1.0	405	10	US-09-814-353-1208	Sequence 1208, Ap
	639	16	1.0	405	10	US-09-814-353-7574	Sequence 7574, Ap
	640	16	1.0	406	10	US-09-814-353-1141	Sequence 1141, Ap
	641	16	1.0	406	10	US-09-814-353-7507	Sequence 7507, Ap
	642	16	1.0	407	9	US-09-960-352-931	Sequence 931, App
	643	16	1.0	407	10	US-09-814-353-1233	Sequence 1233, Ap
	644	16	1.0	407	10	US-09-814-353-1250	Sequence 1250, Ap
	645	16	1.0	407	10	US-09-814-353-7598	Sequence 7598, Ap
	646	16	1.0	407	10	US-09-814-353-7614	Sequence 7614, Ap
	647	16	1.0	409	10	US-09-814-353-1142	Sequence 1142, Ap
	648	16	1.0	409	10	US-09-814-353-1297	Sequence 1297, Ap
	649	16	1.0	409	10	US-09-814-353-7508	Sequence 7508, Ap
	650	16	1.0	409	10	US-09-814-353-7661	Sequence 7661, Ap
	651	16	1.0	410	10	US-09-814-353-1215	Sequence 1215, Ap
	652	16	1.0	410	10	US-09-814-353-7580	Sequence 7580, Ap
c	653	16	1.0	411	15	US-10-029-386-4373	Sequence 4373, Ap
	654	16	1.0	411	16	US-10-424-599-81671	Sequence 81671, A
	655	16	1.0	412	10	US-09-918-995-6491	Sequence 6491, Ap
	656	16	1.0	413	10	US-09-814-353-1202	Sequence 1202, Ap
	657	16	1.0	413	10	US-09-814-353-7568	Sequence 7568, Ap
	658	16	1.0	413	18	US-10-425-115-79311	Sequence 79311, A
	659	16	1.0	416	10	US-09-814-353-1222	Sequence 1222, Ap
	660	16	1.0	416	10	US-09-814-353-1272	Sequence 1272, Ap
	661	16	1.0	416	10	US-09-814-353-7587	Sequence 7587, Ap
	662	16	1.0	416	10	US-09-814-353-7636	Sequence 7636, Ap
c	663	16	1.0	417	9	US-09-764-877-3478	Sequence 3478, Ap
	664	16	1.0	417	16	US-10-131-827-8888	Sequence 8888, Ap
c	665	16	1.0	417	16	US-10-242-515-3478	Sequence 3478, Ap
	666	16	1.0	417	18	US-10-425-115-65607	Sequence 65607, A
	667	16	1.0	418	10	US-09-814-353-1279	Sequence 1279, Ap
	668	16	1.0	418	10	US-09-814-353-1285	Sequence 1285, Ap
	669	16	1.0	418	10	US-09-814-353-7643	Sequence 7643, Ap

	670	16	1.0	418	10	US-09-814-353-7649 Sequence 7649, Ap
	671	16	1.0	418	10	US-09-814-353-14051 Sequence 14051, A
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	673	16	1.0	420	9	US-09-728-445-576 Sequence 576, App
	674	16	1.0	420	10	US-09-814-353-1151 Sequence 1151, Ap
	675	16	1.0	420	10	US-09-814-353-1253 Sequence 1253, Ap
	676	16	1.0	420	10	US-09-814-353-7517 Sequence 7517, Ap
	677	16	1.0	420	10	US-09-814-353-7617 Sequence 7617, Ap
	678	16	1.0	420	10	US-09-814-353-12700 Sequence 12700, A
	679	16	1.0	420	10	US-09-814-353-12701 Sequence 12701, A
	680	16	1.0	420	16	US-10-424-599-76325 Sequence 76325, A
	681	16	1.0	421	10	US-09-918-995-16853 Sequence 16853, A
	682	16	1.0	421	10	US-09-814-353-1213 Sequence 1213, Ap
	683	16	1.0	421	10	US-09-814-353-1238 Sequence 1238, Ap
	684	16	1.0	421	10	US-09-814-353-13953 Sequence 13953, A
	685	16	1.0	422	14	US-10-066-543-2337 Sequence 2337, Ap
	686	16	1.0	423	10	US-09-814-353-14053 Sequence 14053, A
	687	16	1.0	423	16	US-10-424-599-8442 Sequence 8442, Ap
	688	16	1.0	423	18	US-10-674-124A-13998 Sequence 13998, A
	689	16	1.0	424	9	US-09-815-242-2427 Sequence 2427, Ap
	690	16	1.0	424	16	US-10-282-122A-4988 Sequence 4988, Ap
	691	16	1.0	425	10	US-09-814-353-1229 Sequence 1229, Ap
	692	16	1.0	425	10	US-09-814-353-7594 Sequence 7594, Ap
	693	16	1.0	427	10	US-09-814-353-13983 Sequence 13983, A
	694	16	1.0	427	10	US-09-814-353-13985 Sequence 13985, A
	695	16	1.0	427	10	US-09-814-353-14000 Sequence 14000, A
	696	16	1.0	428	10	US-09-814-353-13956 Sequence 13956, A
	697	16	1.0	430	10	US-09-814-353-1261 Sequence 1261, Ap
	698	16	1.0	430	10	US-09-814-353-1268 Sequence 1268, Ap
	699	16	1.0	430	10	US-09-814-353-7625 Sequence 7625, Ap
	700	16	1.0	430	10	US-09-814-353-7632 Sequence 7632, Ap
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	702	16	1.0	432	13	US-10-027-632-298916 Sequence 298916,
	703	16	1.0	432	15	US-10-027-632-57171 Sequence 57171, A
	704	16	1.0	432	15	US-10-027-632-298916 Sequence 298916,
	705	16	1.0	433	10	US-09-814-353-1179 Sequence 1179, Ap
	706	16	1.0	433	10	US-09-814-353-1217 Sequence 1217, Ap
	707	16	1.0	433	10	US-09-814-353-7545 Sequence 7545, Ap
	708	16	1.0	433	10	US-09-814-353-7582 Sequence 7582, Ap
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	710	16	1.0	433	18	US-10-425-115-50661 Sequence 50661, A
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	714	16	1.0	437	10	US-09-814-353-1226 Sequence 1226, Ap
	715	16	1.0	437	10	US-09-814-353-7586 Sequence 7586, Ap
	716	16	1.0	437	10	US-09-814-353-7591 Sequence 7591, Ap
	717	16	1.0	437	10	US-09-814-353-14024 Sequence 14024, A
	718	16	1.0	440	10	US-09-918-995-6809 Sequence 6809, Ap
	719	16	1.0	441	10	US-09-814-353-1258 Sequence 1258, Ap
	720	16	1.0	441	10	US-09-814-353-7622 Sequence 7622, Ap
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	722	16	1.0	443	10	US-09-814-353-1193 Sequence 1193, Ap
	723	16	1.0	443	10	US-09-814-353-7559 Sequence 7559, Ap
c	724	16	1.0	443	16	US-10-242-515-2625 Sequence 2625, Ap
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	726	16	1.0	447	10	US-09-918-995-11990 Sequence 11990, A
	727	16	1.0	447	10	US-09-814-353-14002 Sequence 14002, A
	728	16	1.0	448	10	US-09-814-353-13948 Sequence 13948, A
	729	16	1.0	449	10	US-09-918-995-14542 Sequence 14542, A
	730	16	1.0	449	10	US-09-814-353-13943 Sequence 13943, A
	731	16	1.0	451	10	US-09-814-353-1273 Sequence 1273, Ap
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	733	16	1.0	451	13	US-10-027-632-1350 Sequence 1350, Ap
	734	16	1.0	451	13	US-10-027-632-1351 Sequence 1351, Ap
	735	16	1.0	451	13	US-10-027-632-1352 Sequence 1352, Ap
	736	16	1.0	451	15	US-10-027-632-1350 Sequence 1350, Ap
	737	16	1.0	451	15	US-10-027-632-1351 Sequence 1351, Ap
	738	16	1.0	451	15	US-10-027-632-1352 Sequence 1352, Ap
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c	741	16	1.0	451	16	US-10-085-783A-29367 Sequence 29367, A
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	743	16	1.0	452	9	US-09-864-761-11674 Sequence 11674, A
	744	16	1.0	452	11	US-09-732-627A-3186 Sequence 3186, Ap
	745	16	1.0	453	10	US-09-814-353-14021 Sequence 14021, A
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	747	16	1.0	454	10	US-09-814-353-1267 Sequence 1267, Ap
	748	16	1.0	454	10	US-09-814-353-7631 Sequence 7631, Ap
	749	16	1.0	454	10	US-09-814-353-13992 Sequence 13992, A
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	751	16	1.0	455	10	US-09-814-353-1125 Sequence 1125, Ap
	752	16	1.0	455	10	US-09-814-353-7491 Sequence 7491, Ap
	753	16	1.0	457	10	US-09-814-353-14010 Sequence 14010, A
	754	16	1.0	458	9	US-09-864-761-10601 Sequence 10601, A
	755	16	1.0	458	9	US-09-864-761-13834 Sequence 13834, A
	756	16	1.0	458	10	US-09-814-353-1189 Sequence 1189, Ap
	757	16	1.0	458	10	US-09-814-353-7555 Sequence 7555, Ap
	758	16	1.0	458	10	US-09-814-353-13993 Sequence 13993, A
	759	16	1.0	459	9	US-09-877-156-7 Sequence 7, Appli
	760	16	1.0	459	16	US-10-356-736-27 Sequence 27, Appl
	761	16	1.0	459	16	US-10-274-300-80 Sequence 80, Appl
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	763	16	1.0	460	16	US-10-356-736-25 Sequence 25, Appl
	764	16	1.0	460	16	US-10-356-736-32 Sequence 32, Appl
	765	16	1.0	460	16	US-10-356-736-34 Sequence 34, Appl
	766	16	1.0	460	16	US-10-274-300-78 Sequence 78, Appl
	767	16	1.0	460	16	US-10-274-300-85 Sequence 85, Appl
	768	16	1.0	460	16	US-10-274-300-87 Sequence 87, Appl
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	771	16	1.0	461	13	US-10-027-632-37497 Sequence 37497, A
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	773	16	1.0	461	13	US-10-027-632-63547 Sequence 63547, A
	774	16	1.0	461	13	US-10-027-632-65381 Sequence 65381, A
	775	16	1.0	461	13	US-10-027-632-65382 Sequence 65382, A
	776	16	1.0	461	13	US-10-027-632-297164 Sequence 297164,
	777	16	1.0	461	13	US-10-027-632-297186 Sequence 297186,
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	779	16	1.0	461	15	US-10-027-632-37497 Sequence 37497, A
	780	16	1.0	461	15	US-10-027-632-63546 Sequence 63546, A
	781	16	1.0	461	15	US-10-027-632-63547 Sequence 63547, A
	782	16	1.0	461	15	US-10-027-632-65381 Sequence 65381, A
	783	16	1.0	461	15	US-10-027-632-65382 Sequence 65382, A
	784	16	1.0	461	15	US-10-027-632-297164 Sequence 297164,
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	787	16	1.0	462	16	US-10-356-736-26 Sequence 26, Appl
	788	16	1.0	462	16	US-10-356-736-35 Sequence 35, Appl
	789	16	1.0	462	16	US-10-274-300-79 Sequence 79, Appl
	790	16	1.0	462	16	US-10-274-300-88 Sequence 88, Appl
	791	16	1.0	463	10	US-09-814-353-1163 Sequence 1163, Ap
	792	16	1.0	463	10	US-09-814-353-7529 Sequence 7529, Ap
	793	16	1.0	463	10	US-09-814-353-13906 Sequence 13906, A
	794	16	1.0	463	10	US-09-814-353-13915 Sequence 13915, A
	795	16	1.0	463	16	US-10-356-736-36 Sequence 36, Appl
	796	16	1.0	463	16	US-10-274-300-89 Sequence 89, Appl
	797	16	1.0	464	10	US-09-918-995-15302 Sequence 15302, A
	798	16	1.0	464	10	US-09-814-353-1155 Sequence 1155, Ap
	799	16	1.0	464	10	US-09-814-353-7521 Sequence 7521, Ap
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	803	16	1.0	465	10	US-09-814-353-7544 Sequence 7544, Ap
	804	16	1.0	466	10	US-09-814-353-15805 Sequence 15805, A
	805	16	1.0	466	16	US-10-356-736-30 Sequence 30, Appl
	806	16	1.0	466	16	US-10-356-736-31 Sequence 31, Appl
	807	16	1.0	466	16	US-10-274-300-83 Sequence 83, Appl
	808	16	1.0	466	16	US-10-274-300-84 Sequence 84, Appl
	809	16	1.0	467	10	US-09-814-353-13996 Sequence 13996, A
	810	16	1.0	467	16	US-10-356-736-28 Sequence 28, Appl
	811	16	1.0	467	16	US-10-356-736-29 Sequence 29, Appl
	812	16	1.0	467	16	US-10-356-736-33 Sequence 33, Appl
	813	16	1.0	467	16	US-10-274-300-81 Sequence 81, Appl
	814	16	1.0	467	16	US-10-274-300-82 Sequence 82, Appl
	815	16	1.0	467	16	US-10-274-300-86 Sequence 86, Appl

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	817	16	1.0	469	10	US-09-814-353-7548	Sequence 7548, Ap
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	819	16	1.0	470	9	US-09-864-761-6154	Sequence 6154, Ap
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	823	16	1.0	471	10	US-09-814-353-1191	Sequence 1191, Ap
	824	16	1.0	471	10	US-09-814-353-7557	Sequence 7557, Ap
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	829	16	1.0	475	10	US-09-814-353-1214	Sequence 1214, Ap
	830	16	1.0	475	10	US-09-814-353-7579	Sequence 7579, Ap
	831	16	1.0	475	10	US-09-814-353-13944	Sequence 13944, A
	832	16	1.0	476	10	US-09-814-353-13875	Sequence 13875, A
	833	16	1.0	477	10	US-09-918-995-3093	Sequence 3093, Ap
	834	16	1.0	478	10	US-09-814-353-1290	Sequence 1290, Ap
	835	16	1.0	478	10	US-09-814-353-7654	Sequence 7654, Ap
	836	16	1.0	479	10	US-09-814-353-13965	Sequence 13965, A
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	839	16	1.0	480	10	US-09-918-995-1133	Sequence 1133, Ap
	840	16	1.0	480	10	US-09-918-995-13600	Sequence 13600, A
	841	16	1.0	480	10	US-09-907-969-60	Sequence 60, Appl
	842	16	1.0	480	10	US-09-827-271-60	Sequence 60, Appl
	843	16	1.0	480	10	US-09-814-353-13893	Sequence 13893, A
	844	16	1.0	480	15	US-10-198-053-60	Sequence 60, Appl
	845	16	1.0	480	15	US-10-166-653-13	Sequence 13, Appl
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c	847	16	1.0	482	16	US-10-242-535A-40220	Sequence 40220, A
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	850	16	1.0	483	10	US-09-814-353-7611	Sequence 7611, Ap
	851	16	1.0	483	10	US-09-814-353-13892	Sequence 13892, A
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	855	16	1.0	486	10	US-09-814-353-13975	Sequence 13975, A
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	857	16	1.0	487	10	US-09-814-353-13936	Sequence 13936, A
	858	16	1.0	487	16	US-10-242-535A-36335	Sequence 36335, A
	859	16	1.0	487	16	US-10-085-783A-36335	Sequence 36335, A
	860	16	1.0	488	14	US-10-060-036-3137	Sequence 3137, Ap
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	862	16	1.0	490	10	US-09-814-353-13929	Sequence 13929, A
	863	16	1.0	490	10	US-09-814-353-13967	Sequence 13967, A
	864	16	1.0	490	14	US-10-010-731-19	Sequence 19, Appl
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	866	16	1.0	491	9	US-09-894-924-3	Sequence 3, Appli
	867	16	1.0	491	10	US-09-814-353-1293	Sequence 1293, Ap
	868	16	1.0	491	10	US-09-814-353-7657	Sequence 7657, Ap
	869	16	1.0	491	16	US-10-456-819-3	Sequence 3, Appli
	870	16	1.0	491	17	US-10-688-132-3	Sequence 3, Appli
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	872	16	1.0	493	10	US-09-814-353-14017	Sequence 14017, A
	873	16	1.0	495	10	US-09-814-353-14016	Sequence 14016, A
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	875	16	1.0	496	10	US-09-918-995-21104	Sequence 21104, A
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	877	16	1.0	496	17	US-10-767-701-3473	Sequence 3473, Ap
	878	16	1.0	497	10	US-09-814-353-1283	Sequence 1283, Ap
	879	16	1.0	497	10	US-09-814-353-7647	Sequence 7647, Ap
	880	16	1.0	497	16	US-10-356-736-24	Sequence 24, Appl
	881	16	1.0	497	16	US-10-274-300-77	Sequence 77, Appl
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c	884	16	1.0	498	13	US-10-027-632-62153	Sequence 62153, A
c	885	16	1.0	498	13	US-10-027-632-62154	Sequence 62154, A
c	886	16	1.0	498	13	US-10-027-632-62155	Sequence 62155, A
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c	892	16	1.0	498	15	US-10-027-632-62153	Sequence 62153, A
c	893	16	1.0	498	15	US-10-027-632-62154	Sequence 62154, A
c	894	16	1.0	498	15	US-10-027-632-62155	Sequence 62155, A
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	898	16	1.0	499	16	US-10-424-599-47065	Sequence 47065, A
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	900	16	1.0	500	10	US-09-814-353-14022	Sequence 14022, A
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c	902	16	1.0	500	16	US-10-242-535A-51633	Sequence 51633, A
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	904	16	1.0	502	10	US-09-814-353-1298	Sequence 1298, Ap
	905	16	1.0	502	10	US-09-814-353-7662	Sequence 7662, Ap
	906	16	1.0	502	10	US-09-814-353-13972	Sequence 13972, A
	907	16	1.0	502	16	US-10-242-535A-16202	Sequence 16202, A
	908	16	1.0	502	16	US-10-085-783A-16202	Sequence 16202, A
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	912	16	1.0	504	10	US-09-814-353-1123	Sequence 1123, Ap
	913	16	1.0	504	10	US-09-814-353-1187	Sequence 1187, Ap
	914	16	1.0	504	10	US-09-814-353-7489	Sequence 7489, Ap
	915	16	1.0	504	10	US-09-814-353-7553	Sequence 7553, Ap
	916	16	1.0	504	10	US-09-814-353-13966	Sequence 13966, A
	917	16	1.0	504	18	US-10-425-115-131391	Sequence 131391,
	918	16	1.0	505	10	US-09-814-353-1224	Sequence 1224, Ap
	919	16	1.0	505	10	US-09-814-353-7589	Sequence 7589, Ap
	920	16	1.0	506	10	US-09-814-353-13933	Sequence 13933, A
	921	16	1.0	507	10	US-09-814-353-1154	Sequence 1154, Ap
	922	16	1.0	507	10	US-09-814-353-1225	Sequence 1225, Ap
	923	16	1.0	507	10	US-09-814-353-7520	Sequence 7520, Ap
	924	16	1.0	507	10	US-09-814-353-7590	Sequence 7590, Ap
	925	16	1.0	507	14	US-10-010-731-10	Sequence 10, Appl
	926	16	1.0	508	10	US-09-814-353-13940	Sequence 13940, A
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	929	16	1.0	509	10	US-09-814-353-13978	Sequence 13978, A
	930	16	1.0	510	10	US-09-814-353-1287	Sequence 1287, Ap
	931	16	1.0	510	10	US-09-814-353-7651	Sequence 7651, Ap
	932	16	1.0	510	10	US-09-814-353-13960	Sequence 13960, A
	933	16	1.0	510	16	US-10-242-535A-15058	Sequence 15058, A
	934	16	1.0	510	16	US-10-085-783A-15058	Sequence 15058, A
	935	16	1.0	511	10	US-09-814-353-13963	Sequence 13963, A
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	937	16	1.0	511	15	US-10-027-632-13710	Sequence 13710, A
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	939	16	1.0	513	10	US-09-814-353-7513	Sequence 7513, Ap
	940	16	1.0	513	10	US-09-814-353-13979	Sequence 13979, A
	941	16	1.0	513	10	US-09-814-353-14049	Sequence 14049, A
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c	955	16	1.0	517	15	US-10-027-632-191218	Sequence 191218,
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	958	16	1.0	519	10	US-09-814-353-7552	Sequence 7552, Ap
	959	16	1.0	521	10	US-09-814-353-1181	Sequence 1181, Ap
	960	16	1.0	521	10	US-09-814-353-7547	Sequence 7547, Ap
	961	16	1.0	521	10	US-09-814-353-13974	Sequence 13974, A

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966	16	1.0	524	10	US-09-814-353-1228	Sequence 1228, Ap
967	16	1.0	524	10	US-09-814-353-7515	Sequence 7515, Ap
968	16	1.0	524	10	US-09-814-353-7581	Sequence 7581, Ap
969	16	1.0	524	10	US-09-814-353-7593	Sequence 7593, Ap
970	16	1.0	525	10	US-09-814-353-1140	Sequence 1140, Ap
971	16	1.0	525	10	US-09-814-353-7506	Sequence 7506, Ap
972	16	1.0	525	10	US-09-814-353-13959	Sequence 13959, A
973	16	1.0	526	9	US-09-878-178-853	Sequence 853, App
974	16	1.0	526	13	US-10-046-935-853	Sequence 853, App
975	16	1.0	526	14	US-10-146-502-853	Sequence 853, App
c 976	16	1.0	526	17	US-10-437-963-34444	Sequence 34444, A
977	16	1.0	527	10	US-09-814-353-13876	Sequence 13876, A
c 978	16	1.0	527	11	US-09-969-034-4399	Sequence 4399, Ap
979	16	1.0	528	9	US-09-998-598-1386	Sequence 1386, Ap
c 980	16	1.0	529	9	US-09-867-701-6460	Sequence 6460, Ap
981	16	1.0	529	10	US-09-814-353-15777	Sequence 15777, A
c 982	16	1.0	529	11	US-09-969-034-3544	Sequence 3544, Ap
983	16	1.0	529	18	US-10-425-115-5511	Sequence 5511, Ap
984	16	1.0	531	9	US-09-884-441-5	Sequence 5, Appli
c 985	16	1.0	531	9	US-09-974-300-6343	Sequence 6343, Ap
986	16	1.0	531	10	US-09-907-969-5	Sequence 5, Appli
987	16	1.0	531	10	US-09-827-271-5	Sequence 5, Appli
988	16	1.0	531	15	US-10-198-053-5	Sequence 5, Appli
c 989	16	1.0	532	18	US-10-425-115-58724	Sequence 58724, A
990	16	1.0	533	10	US-09-814-353-1212	Sequence 1212, Ap
991	16	1.0	533	10	US-09-814-353-7578	Sequence 7578, Ap
992	16	1.0	536	10	US-09-814-353-13878	Sequence 13878, A
993	16	1.0	537	13	US-10-027-632-195778	Sequence 195778,
994	16	1.0	537	13	US-10-027-632-195779	Sequence 195779,
995	16	1.0	537	15	US-10-027-632-195778	Sequence 195778,
996	16	1.0	537	15	US-10-027-632-195779	Sequence 195779,
997	16	1.0	538	10	US-09-814-353-1234	Sequence 1234, Ap
998	16	1.0	538	10	US-09-814-353-7599	Sequence 7599, Ap
c 999	16	1.0	539	13	US-10-027-632-243606	Sequence 243606,
c1000	16	1.0	539	15	US-10-027-632-243606	Sequence 243606,

ALIGNMENTS

RESULT 1
US-10-425-114-3830
; Sequence 3830, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3830
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700342511_FLI
US-10-425-114-3830

Query Match 1.2%; Score 20; DB 16; Length 1022;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 993 AGAAACAGCTCTAGTCAACA 1012
||||||||||||||||||||
Db 590 AGAAACAGCTCTAGTCAACA 609

RESULT 2
US-10-425-115-67965
; Sequence 67965, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 67965
; LENGTH: 1718
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_161981C.1
US-10-425-115-67965

Query Match 1.2%; Score 20; DB 18; Length 1718;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 993 AGAAACAGCTCTAGTCAACA 1012
||||||||||||||||||||
Db 976 AGAAACAGCTCTAGTCAACA 995

RESULT 3
US-09-764-891-9479/c
; Sequence 9479, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9479
; LENGTH: 31140
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-9479

Query Match 1.2%; Score 20; DB 10; Length 31140;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 534 TGAAACTGCTTTAAAACTCC 553
||||||||||||||||||||
Db 25120 TGAAACTGCTTTAAAACTCC 25101

RESULT 4
US-10-205-428-860/c
; Sequence 860, Application US/10205428
; Publication No. US20030108907A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA117C1

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;  CURRENT APPLICATION NUMBER: US/10/205,428
;  CURRENT FILING DATE:  2002-07-26
;  PRIOR APPLICATION NUMBER: 09/764,892
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/218,290
;  PRIOR FILING DATE: 2000-07-14
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1019
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 860
;   LENGTH: 31140
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-205-428-860

  Query Match             1.2%;  Score 20;  DB 15;  Length 31140;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        534 TGAAACTGCTTTAAAACTCC 553
              ||||||||||||||||||||
Db      25120 TGAAACTGCTTTAAAACTCC 25101


RESULT 5
US-10-741-601-16635
; Sequence 16635, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16635
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-16635

  Query Match             1.2%;  Score 19;  DB 17;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 43;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1206 TGTATTTTGCATATATGGT 1224
              |||||||||||||||||||
Db        179 TGTATTTTGCATATATGGT 197


RESULT 6
US-10-276-774-400/c
; Sequence 400, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  APPLICANT:  Tang, Y, Tom et al
;  TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-030
;  CURRENT APPLICATION NUMBER: US/10/276,774
;  CURRENT FILING DATE:  2002-11-18
;  PRIOR APPLICATION NUMBER: 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 2700
;  SOFTWARE: Custom
; SEQ ID NO 400
;   LENGTH: 453
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-276-774-400

  Query Match             1.2%;  Score 19;  DB 16;  Length 453;
  Best Local Similarity   100.0%;  Pred. No. 46;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        703 CTTCTTGGTTCTGTTGAGG 721
              |||||||||||||||||||
Db        187 CTTCTTGGTTCTGTTGAGG 169


RESULT 7
US-10-424-599-8986/c
; Sequence 8986, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 8986
;   LENGTH: 656
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(656)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_108124C.1
US-10-424-599-8986

  Query Match             1.2%;  Score 19;  DB 16;  Length 656;
  Best Local Similarity   100.0%;  Pred. No. 48;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        635 TTGCACCAAAACATTATTT 653
              |||||||||||||||||||
Db        266 TTGCACCAAAACATTATTT 248


RESULT 8
US-10-424-599-125442
; Sequence 125442, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
```

```
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 125442
;   LENGTH: 983
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(983)
;   OTHER INFORMATION: unsure at all n locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_84284C.1
US-10-424-599-125442

  Query Match             1.2%;  Score 19;  DB 16;  Length 983;
  Best Local Similarity   100.0%;  Pred. No. 50;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        526 TTGACCTTTGAAACTGCTT 544
              ||||||||||||||||||
Db         89 TTGACCTTTGAAACTGCTT 107


RESULT 9
US-10-282-122A-9460/c
; Sequence 9460, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
;  APPLICANT:  Yamamoto, Robert
;  APPLICANT:  Forsyth, R.
;  APPLICANT:  Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:  2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9460
;   LENGTH: 1584
;   TYPE: DNA
;   ORGANISM: Bacillus anthracis
US-10-282-122A-9460

  Query Match             1.2%;  Score 19;  DB 16;  Length 1584;
  Best Local Similarity   100.0%;  Pred. No. 51;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        591 TAATAATGTCTTCAGATAC 609
              ||||||||||||||||||
Db       1564 TAATAATGTCTTCAGATAC 1546


RESULT 10
US-10-437-963-76086
; Sequence 76086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 76086
;   LENGTH: 1719
;   TYPE: DNA
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_76111C.1
US-10-437-963-76086

  Query Match             1.2%;  Score 19;  DB 17;  Length 1719;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        326 GGCCTGACAGTGGTCTTTC 344
              ||||||||||||||||||
Db        341 GGCCTGACAGTGGTCTTTC 359


RESULT 11
US-08-781-986A-107
; Sequence 107, Application US/08781986A
; Publication No. US20030054436A1
;  GENERAL INFORMATION:
;    APPLICANT:  Charles Kunsch
;    TITLE OF INVENTION:  Staphylococcus aureus Polynucleotides and Sequences
;    NUMBER OF SEQUENCES:  5255
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockville
;      STATE:  Maryland
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.4Mb storage
;      COMPUTER:  HP Vectra 486/33
;      OPERATING SYSTEM:  MSDOS version 6.2
;      SOFTWARE:  ASCII Text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/781,986A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Bob
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  PB248PP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 309-8504
;      TELEFAX:  (301) 309-8512
;  INFORMATION FOR SEQ ID NO:  107:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2488 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-781-986A-107

  Query Match             1.2%;  Score 19;  DB 8;  Length 2488;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        923 AATATCAATCAAAATATTC 941
              |||||||||||||||||||
Db       1354 AATATCAATCAAAATATTC 1372


RESULT 12
US-10-329-624-107
; Sequence 107, Application US/10329624
; Publication No. US20040043037A1
;   GENERAL INFORMATION:
;        APPLICANT: Charles Kunsch
;                   Gil H. Choi
;                   Patrick S. Dillon
;                   Craig A. Rosen
;                   Steven C. Barash
;                   Michael R. Fannon
;        TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;        NUMBER OF SEQUENCES: 5256
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: Maryland
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;             COMPUTER: HP Vectra 486/33
;             OPERATING SYSTEM: MSDOS version 6.2
;             SOFTWARE: ASCII Text
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/329,624
;             FILING DATE: 27-Dec-2002
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/956,171
;             FILING DATE: October 20, 1997
;             APPLICATION NUMBER: 60/009,861
;             FILING DATE: January 5, 1996
;             APPLICATION NUMBER: 08/781,986
;             FILING DATE: January 3, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Mark J. Hyman
;             REGISTRATION NUMBER: 46,789
;             REFERENCE/DOCKET NUMBER: PB248P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (240) 314-1224
;             TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 107:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2488 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;           SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-329-624-107

  Query Match             1.2%;  Score 19;  DB 16;  Length 2488;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        923 AATATCAATCAAAATATTC 941
              |||||||||||||||||||
Db       1354 AATATCAATCAAAATATTC 1372


RESULT 13
US-10-424-599-117318
; Sequence 117318, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 117318
;   LENGTH: 2625
;   TYPE: DNA
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_76949C.1
US-10-424-599-117318

  Query Match             1.2%;  Score 19;  DB 16;  Length 2625;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         50 TTTTTTTCTTGATTTGCGG 68
              |||||||||||||||||||
Db        432 TTTTTTTCTTGATTTGCGG 450


RESULT 14
US-10-741-601-5741
; Sequence 5741, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  STENOSIS, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001500
;  CURRENT APPLICATION NUMBER: US/10/741,601
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 26415
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5741
;   LENGTH: 59247
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-601-5741

  Query Match             1.2%;  Score 19;  DB 17;  Length 59247;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        689 CTGTTGGAGCTCCTCTTCT 707
              |||||||||||||||||||
Db      10349 CTGTTGGAGCTCCTCTTCT 10367
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RESULT 15
US-10-741-601-5641
; Sequence 5641, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5641
; LENGTH: 112486
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112486)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5641

Query Match 1.2%; Score 19; DB 17; Length 112486;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        689 CTGTTGGAGCTCCTCTTCT 707
              ||||||||||||||||||| 
Db     100878 CTGTTGGAGCTCCTCTTCT 100896
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Search completed: November 9, 2004, 10:30:35
Job time : 1341 secs